

From: Borin, Michael
Sent: Friday, September 09, 2005 4:23 PM
To: STIC-Biotech/ChemLib
Subject: Search request: 10/617217

Examiner: M.Borin
AU: 1631
Mailbox: 2C70
Office: Remsen 2A55
Tel.: 20713

RE: 10617217; EST

ME
Please search nucleic acid SEQ ID NO: 88.

Thank you

na 2717

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Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CGN



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 165349

TO: Michael Borin
Art Unit: 1631
Location: REM/2A55/2C70
Serial Number: 10/617217

Friday, September 23, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

PRIOR APPLICATION NUMBER: PCT/US00/22350
 PRIOR FILING DATE: 2000-08-15
 PRIOR APPLICATION NUMBER: 60/148,759
 PRIOR FILING DATE: 1999-08-16
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 1860
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-768-826-15

Query Match 67.6%; Score 1835.8; DB 9; Length 1860;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1837; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1822 ATAGTTGCAAGAGCTTTATATGCTTATTAATGAAG 1860

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RESULT 6
 US-10-874-484-15
 Sequence 15, Application US/10874484
 Publication No. US20040235113A1
 GENERAL INFORMATION:

Box 11, N.
10/6/7217
Seq ID 88

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

CM nucleic - nucleic search, using SW model

Run on: September 22, 2005, 23:45:41; Search time 11587 Seconds
(without alignments)

11362.115 Million cell updates/sec

Title: US-10-617-217a-88

Perfect score: 2717

Sequence: 1 aaagaagaacagaaagcc.....ataaagctttattcttc 2717

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Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_da.*
2: gb_hcg.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
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13: gb_pl.*
14: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2717	100.0	2717	9	AB097022 Homo sapi
3	2667	98.2	3453	9	AY304583 Homo sapi
4	2666	98.1	124310	2	AC008587 Homo sapi
5	2666	98.1	147140	2	AC010226 Homo sapi
6	2661	98.0	155276	2	AC091992 Homo sapi
7	2546	93.7	3335	9	AY304584 Homo sapi
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9	981	36.1	1149	9	AY275836 Homo sapi
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13	808	29.7	808	9	AB091054 Homo sapi
14	725	26.7	725	9	AB091054 Homo sapi
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17	676	24.9	770	11	BY210323 Homo sapi
18	650	23.9	1215	9	AY304581 Homo sapi
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C	22	510	18.8	3264	10	AY275837	Mus muscu
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C	24	476	17.5	533	6	BD126044	Primer fo
C	25	467	17.2	880	10	AB100441	Mus muscu
C	26	431	15.9	699	10	AY268050	Mus muscu
C	27	416	15.3	420	9	AB002443	Homo sapi
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ALIGNMENTS

RESULT 1
LOCUS BD170656
DEFINITION NF-kappa B activation gene.
ACCESSION BD170656
VERSION BD170656.1 GI:27876468
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2717)
Matsuda, A., Honda, G., Muramatsu, S. and Nagano, Y.
NF-kappa B activation gene
Patent: WO 02053737-A 44-11-JUL-2002;
ASAHI KASEI CORP, AKIO MATSUDA, GOICHI HONDA, SHUJI MURAMATSU, YUKIKO NAGANO
COMMENT OS Homo sapiens (human)
PN WO 02053737-A/44
PD 11-JUL-2002
PF 25-DEC-2001 WO 2001JP011389
PR 28-DEC-2000 JP 00P 402288, 26-MAR-2001 JP 01P 088912 PR
24-AUG-2001 JP 01P 254018
PI AKIO MATSUDA, GOICHI HONDA, SHUJI MURAMATSU, YUKIKO NAGANO
C12N15/12, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10,
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AC136875, A61K38/02, A61K39/395, A61K45/00, A61K48/00, A61P29/00, PC
A61P35/00
PC A61P37/00, C12Q1/68, C12N9/00, G01N33/15, G01N33/50, G01N33/53, PC
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CC NF-kappa B activation gene
FH Key location/Qualifiers
FT CDS location/Qualifiers
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/db_xref="taxon:9606"

FEATURES

source
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GGAAGCTTAAATTAATTTCTTCTCTCTCTTGGGTAAAGCAAGTGTG 180
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Qy 2701 AAATGTTTATATCTTT 2717

Db 2701 AAATGTTTATATCTTT 2717

RESULT 2
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LOCUS Homo sapiens mRNA for putative NFKB activating protein, complete cds, clone: 502.
ACCESSION AB097022
VERSION AB097022.1 GI:31455498
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Matsuda, A., Suzuki, Y., Honda, G., Muramatsu, S., Mutsuzaki, O., Nagano, Y., Doi, T., Shimotohno, K., Harada, T., Nishida, E., Hayashi, H. and Sugano, S.
TITLE Large-scale identification and characterization of human genes that activate NF-kappaB and MAPK signaling pathways
JOURNAL Oncogene 22 (21), 3307-3318 (2003)
MEDLINE 12761501
PUBMED 22646590
REFERENCE 2 (bases 1 to 2717)
AUTHORS Matsuda, A., Suzuki, Y., Honda, G., Muramatsu, S., Mutsuzaki, O., Nagano, Y., Harada, T., Nishida, E., Hayashi, H. and Sugano, S.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-2002) Yutaka Suzuki, The Institute of Medical Science, The University of Tokyo, Minatoku Shirokanedai 4-6-1, Tokyo, Tokyo 108-8639, Japan (E-mail: yusuzuki@ime.u-tokyo.ac.jp, Tel: 81-3-5449-5343, Fax: 81-3-5449-5416)
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VERSION AY304583.1 GI:37677664
KEYWORDS

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 AUTHORS Hardy, M.P., McGettrick, A.F., Eideback, M. and O'Neill, L.A.J.
 TITLE Identification of a novel variant of the Toll-like receptor adaptor protein TIRAP3
 JOURNAL 2 (bases 1 to 3453)
 REFERENCE Hardy, M.P., McGettrick, A.F. and O'Neill, L.A.J.
 AUTHORS Direct Submission
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AC008587.5 GI:13699388
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
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Direct Submision
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:7708968.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 404250
Center clone name: CIT-HSPC_570H22
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Consensus quality: 113349 bases at least Q30
Consensus quality: 114811 bases at least Q20
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Estimated insert size: 122110; sum-of-coverage gel estimation
Quality coverage: 7.16 in Q20 bases; pulse field gel estimation
Quality coverage: 11.95 in Q20 bases; sum-of-coverage estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1107
1106: gap of unknown length
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5211: contig of 1042 bp in length
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DEFINITION Homo-sapiens chromosome 5 clone CTC-286N18, complete sequence.
AC010226
VERSION AC010226.5 GI:13162506
KEYWORDS HTG
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 147140)
REFERENCE DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS Direct Submision
TITLES Unpublished
JOURNAL 2 (bases 1 to 147140)
REFERENCE DOE Joint Genome Institute.
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JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 147140)
REFERENCE DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS Direct Submision
TITLES Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
Of Feb 28, 2001 this sequence version replaced gi:925616.
DATE Sequence produced by DOE Joint Genome Institute
JOURNAL www.jgi.doe.gov
COMMENT Finishing completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.5.
STS Content:
WI-5151 G02868
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DEFINITION 6 unordered pieces.
AC091992
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VERSION      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155276)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
2 (bases 1 to 155276)
DOE Joint Genome Institute.
Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 25, 2001 this sequence version replaced gi:14333928.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 441299
Center clone name: RPCI-11_90P14
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Summary Statistics
Consensus quality: 151184 bases at least Q40
Consensus quality: 153297 bases at least Q30
Consensus quality: 153815 bases at least Q20
Estimated insert size: 159350; agarose-fp estimation
Estimated insert size: 154776; sum-of-coverage estimation
Quality coverage: 5.9 in Q20 bases; agarose-fp estimation
Quality coverage: 6.07 in Q20 bases; sum-of-coverage estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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7360
7459: gap of unknown length
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17306: contig of 9847 bp in length
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 ACCESSION AY04584
 VERSION AY04584.1 GI:37677666
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 SOURCE
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 REFERENCES
 1 (bases 1 to 3335)
 Hardy,M.P., McGettrick,A.F., Bjedack,M. and O'Neill,L.A.J.
 Identification of a novel variant of the Toll-like receptor adaptor
 protein TIRAP3
 JOURNAL Unpublished
 2 (bases 1 to 3335)
 Hardy,M.P., McGettrick,A.F. and O'Neill,L.A.J.
 Direct Submision
 JOURNAL Submitted (23-MAY-2003) Biochemistry, Trinity College Dublin,
 College Green, Dublin 2, Ireland
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Matches 2547; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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ACCESSION	AY275836				
VERSION	AY275836.1				
KEYWORDS					
SOURCE	Homo sapiens (human)				

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1 (bases 1 to 1149)	Bin, L. H., Xu, L. G. and Shu, H. B.	TIRP, a Novel Toll/Interleukin-1 receptor (TIR) Domain-containing Adapter Protein Involved in TIR Signaling	J. Biol. Chem. 278 (27), 24526-24532 (2003)	22716271		2 (bases 1 to 1149)	Bin, L. H., Xu, L. G. and Shu, H. B.	Direct Submission			
				12721283				Submitted (14-Apr-2003)	Immunology, National Jewish Medical and Research Center, 1400 Jackson Street, K516c, Denver, CO 80206, USA		
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ACCESSION	Sequence 3459 from Patent Bpl396543.			linear	PAT 17-MAR-2004
VERSION	CQ783319				
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SOURCE	.				
ORGANISM	Homo sapiens (human)				
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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Makamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
Koga, H.
Primers for synthesizing full length cDNA clones and their use
Patent: EP 1396543-A 3459 10-MAR-2004;
Research Association for Biotechnology (JP)
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ORIGIN

Query Match 32.4%; Score 880.6; DB 6; Length 1687;
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102 ATATTATAATGGGATGCGGAAGTCTAAATAAATTCCTGCGCTCTTCTCTCTTGG 161
861 ATATTATAATGGGATGCGGAAGTCTAAATAAATTCCTGCGCTCTTCTCTCTTGG 920
162 GGTAAAGGCAAGTGTGATACAAATCCAGATATCATGAGTCAAGATTCGAAGTCT 221
921 GGTAAAGGCAAGTGTGATACAAATCCAGATATCATGAGTCAAGATTCGAAGTCT 980
222 GAAGATCTATCTCTTGTGATATGCTGCGACAGCAATACAAAGAGGGGCGCAAGGA 281
981 GAAGATCTATCTCTTGTGATATGCTGCGACAGCAATACAAAGAGGGGCGCAAGGA 1040
282 AAGCAGAGGAGCTCAGAGCGTGAAGAGATGTTTGAAGAAGAGCTGAAGAAGGTG 341
1041 AAGCAGAGGAGCTCAGAGCGTGAAGAGATGTTTGAAGAAGAGCTGAAGAAGGTG 1100
342 TTCCTCAATTTGTGATATGATGACAGAGATGACAGATGAAGCCCTCAGAGTCCAG 401
1101 TTCCTCAATTTGTGATATGATGACAGAGATGACAGATGAAGCCCTCAGAGTCCAG 1160
402 AATCTGCTACAGATGATCTTGTATCAAAACCCGGAATAATCTTTGCTGAGATGCAATCT 461
1161 AATCTGCTACAGATGATCTTGTATCAAAACCCGGAATAATCTTTGCTGAGATGCAATCT 1220
462 GGCAGACAGCATTTACAGATTAGATGATGCTGTAAATGGGTCTGCATGACAAATCTTA 521
1221 GGCAGACAGCATTTACAGATTAGATGATGCTGTAAATGGGTCTGCATGACAAATCTTA 1280
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582 ATGAATCTCGTTAAACAGGACATATAATCAACTCTGTATACCAATGGGCGCCCTGAAC 641
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Db 1461 GAAAGTCGTGATTTCTTACCAAGTAGAAGAAATTTTTCAGAGTCTGTGTATTAAGACA 1520
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Db 1521 CAACAACCTATATGGAAGAGACAAAGAAATATGATGACAAAGACATTTATGCGTAGAT 1580
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Db 1641 GAAAGCAGTTCTTGAAGAAATGTTTAAATTAAGAGAGCTTCACTT 1687

RESULT 11
BD127586
LOCUS BD127586 1687 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127586
VERSION BD127586.1 GI:23222531
KEYWORDS JP 2002017375-A/3017.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1687)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Makamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
Koga, H.
Primers for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3017 22-JAN-2002;
JOURNAL HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017375-A/3017
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUOT OTSUKI, HISASHI KOGA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12P1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
PC Primer for synthesizing full-length cDNA and use thereof PH Key

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1. 1687
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ORIGIN

Query Match 32.4%; Score 880.6; DB 6; Length 1687;
Best Local Similarity 99.5%; Pred. No. 5.2e-171;
Matches 883; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

42 TCGCCTGCAGATTGAAAAAAGAAATGCTGAGAAATACATAAAGTTTCCTCTTCTGCTTGG 101
801 TGGCCTATTGATTGAAAAAAGAAATGCTGAGAAATACATAAAGTTTCCTCTTCTGCTTGG 860
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861 ATATTATAATGGGATGCGGAAGTCTAAATAAATTCCTGCGCTCTTCTCTCTTGG 920
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921 GGTAAAGGCAAGTGTGATACAAATCCAGATATCATGAGTCAAGATTCGAAGAGTCT 980

QY 222 GAAAGTCTATCTTGTGTATGTTGCTGAGCACAGCAATACACAGAGGGGCCAACAGCA 281
 DB 981 GAAAGTCTATCTTGTGTATGTTGCTGAGCACAGCAATACACAGAGGGGCCAACAGCA 1040
 QY 282 AAGCAGAGGGAGCTCCAGAGCGGTGAGAGAGATGTTGAAAGAAAGCTAAAGAGGTG 341
 DB 1041 AAGCAGAGGGAGCTCCAGAGCGGTGAGAGAGATGTTGAAAGAAAGCTAAAGAGGTG 1100
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 DB 1101 TTCCTCAATTTGTGTATGTTGATGAGAGATGACACAGATGAGAGCCCTCAGAGTCCAG 1160
 QY 402 AATCTGCTACAAAGATGATCTTTGATCAAAACCCGGAATATCTTTGCTGAGATGCCATGT 461
 DB 1161 AATCTGCTACAAAGATGATCTTTGATCAAAACCCGGAATATCTTTGCTGAGATGCCATGT 1220
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 DB 1221 GGCAGACAGCATTTTACAGAAATTTAGATGATGCTGTAAATGGGTCTGCATGAGCAATCTTA 1280
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 DB 1341 ATGAATCCCGTTTACAGGACGATTAATCAACTCTGTATTAACCATGCGGCCCTGTAAC 1400
 QY 642 AATCCCTTCCCGGAGAAAGACTCCCTTCCCTTCCCAACCATCAATGCTTTAGAGAA 701
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 DB 1581 GAAACATATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1640
 QY 882 GAAAGCAGTTTCTTGAATGTTTAAATTTAAAGAGAGTCTTCACTT 928
 DB 1641 GAAAGCAGTTTCTTGAATGTTTAAATTTAAAGAGAGTCTTCACTT 1687

RESULT 12
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 LOCUS Homo sapiens cDNA FLJ90737 f18, clone PLACE1010827, weakly similar
 DEFINITION to COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR.

AK075218
 VERSION AK075218.1 GI:22761164
 KEYWORDS oligo capping; f18 (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS Iisogai, T., Oca, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
 Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
 Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
 Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y.,
 Aoeuka, S., Sasaki, N., Hatcori, A., Okumura, K., Iwayanagi, T. and
 Niimoriya, K.
 NEDO human cDNA sequencing project
 Unpublished
 JOURNAL
 REFERENCE
 AUTHORS Iisogai, T. and Otsuki, T.
 TITLE Direct Submission

JOURNAL

Submitted (25-MAR-2002) Takao Iisogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kitarazu, Chiba 292-0812, Japan
 (E-mail:genomics@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;
 Research Association for Biotechnology; cDNA library construction;
 Institute of Medical Science, University of Tokyo, Laboratory of
 Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
 sequencing and clone selection; Helix Research Institute (supported
 by Japan Key Technology Center etc.).
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CDS

Query Match 32.4%; Score 880.6; DB 9; Length 1687;
 Best Local Similarity 99.5%; Pred. No. 5,2e-171;
 Matches 883; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ORIGIN

QY 42 TCGCTGAGATTTGAAAGAAATGCTGAGAAATCATATAGTTTCCTTCTGCTTGG 101
 DB 801 TGGCCTATTTGATGTAAGAAAGAAATGCTGAGAAATCATATAGTTTCCTTCTGCTTGG 860
 QY 102 ATATTATTAATGGGATGCGGAAAGCTTAAATTAATTCCTGCTCTCTCTTGG 161
 DB 861 ATATTATTAATGGGATGCGGAAAGCTTAAATTAATTCCTGCTCTCTCTTGG 920
 QY 162 GGTAAAGGCAAGTGTGATTAACAATGTCAGATATCATAGTCAATTCAGAAAGTCT 221
 DB 921 GGTAAAGGCAAGTGTGATTAACAATGTCAGATATCATAGTCAATTCAGAAAGTCT 980
 QY 222 GAAAGTCTATCTTGTGTATGTTGCTGAGACAGCATATCAACAGAGGGCCACAGCA 281
 DB 981 GAAAGTCTATCTTGTGTATGTTGCTGAGACAGCATATCAACAGAGGGCCACAGCA 1040
 QY 282 AAGCAGAGGGAGCTCAGAGCGTGAAGAGATGTTTGAAGAAAGAGTGAAGAGGTG 341
 DB 1041 AAGCAGAGGGAGCTCAGAGCGTGAAGAGATGTTTGAAGAAAGAGTGAAGAGGTG 1100
 QY 342 TTCCTCAATTTGTGTATGTTGATGAGAGATGACACAGATGAGAGCCCTCAGAGTCCAG 401
 DB 1101 TTCCTCAATTTGTGTATGTTGATGAGAGATGACACAGATGAGAGCCCTCAGAGTCCAG 1160
 QY 402 AATCTGCTACAAAGATGATCTTTGATCAAAACCCGGAATATCTTTGCTGAGATGCCATGT 461
 DB 1161 AATCTGCTACAAAGATGATCTTTGATCAAAACCCGGAATATCTTTGCTGAGATGCCATGT 1220
 QY 462 GGCAGACAGCATTTTACAGAAATTTAGATGATGCTGTAAATGGGTCTGCATGAGCAATCTTA 521
 DB 1221 GGCAGACAGCATTTTACAGAAATTTAGATGATGCTGTAAATGGGTCTGCATGAGCAATCTTA 1280
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 DB 1341 ATGAATCCCGTTTACAGGACGATTAATCAACTCTGTATTAACCATGCGGCCCTGTAAC 1400

QY 642 AATCCCTTCCCGAGAAAGACCTCTTGGCCCTCAACATCATGCTTAGAGAA 701
|||||
Db 1401 AATCCCTTCCCGAGAAAGACCTCTTGGCCCTCAACATCATGCTTAGAGAA 1460
QY 702 GAAAGTCGTGATTTCTTACACAGTAAGAAATTTTTCAGAGTCTGTATTAAGAC 761
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Db 1461 GAAAGTCGTGATTTCTTACACAGTAAGAAATTTTTCAGAGTCTGTATTAAGAC 1520
QY 762 CAACAACATTAATGAAAGACAAAGAAATATGTCACAAATTTATTTGCTAGAT 821
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Db 1581 GAAACATTAATGATGCTGCTCTTGTATTAACCAATGATTAATCTTCACTGA 1640
QY 882 GAAAGCATTTCTAGAGAAATGTTTAAATTAAGAGATCTTCACTT 928
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Db 1641 GAAAGCATTTCTAGAGAAATGTTTAAATTAAGAGATCTTCACTT 1687

RESULT 13
AB109098 808 bp mRNA linear PRI 02-OCT-2003
LOCUS Homo sapiens TICAM-2 mRNA for TIR-containing adapter molecule-2,
DEFINITION complete cds.
ACCESSION AB109098
VERSION AB109098.1 GI:37360901
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Oshiumi, H., Sasaki, M., Shida, K., Fujita, T., Matsumoto, M. and Seya, T.
TITLE TICAM-2: a bridging adapter recruiting to Toll-like receptor 4
JOURNAL J. Biol. Chem. (2003) In press
2. (bases 1 to 808)
Oshiumi, H., Shida, K., Matsumoto, M. and Seya, T.
Direct Submision
Submitted (22-APR-2003) Hiroyuki Oshiumi, Osaka University,
Department of Biology, Graduate School of Science, Machikaneyama
1-1, Toyonaka, Osaka 560-0043, Japan
(E-mail: oshiumi@bio.sci.osaka-u.ac.jp, Tel: 81-6-6850-5432,
Fax: 81-6-6850-5440)

FEATURES
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Location/Qualifiers
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ORIGIN
Query Match 29.7%; Score 808; DB 9; Length 808;
Best local Similarity 100.0%; Pred. No. 5, 3e-156;
Matches 808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GCTGACTGTGTGGCGCTCGCTGCAGATTGAAAGAAATGCTGAGAAATACATAAAGTT 84

Db 1 GCTGACTGTGTGGCGCTCGCTGCAGATTGAAAGAAATGCTGAGAAATACATAAAGTT 60
QY 85 TTTCCTCTTCTGCTTGGATTTATTAATGGGATATGGGAAAGCTAAATTAATTCCTGCC 144
61 TTTCCTCTTCTGCTTGGATTTATTAATGGGATATGGGAAAGCTAAATTAATTCCTGCC 120
QY 145 CTCTTCTCTCTCTTGGGGTAAAGGACAGTGTGATCAAGTCCAGATATCATAGT 204
121 CTCTTCTCTCTCTTGGGGTAAAGGACAGTGTGATCAAGTCCAGATATCATAGT 180
Db 205 CAGATTCAGAAAGTCTGAAGTCTATCTTGTATATTTGCTGAGCAGACATACAA 264
181 CAGATTCAGAAAGTCTGAAGTCTATCTTGTATATTTGCTGAGCAGACATACAA 240
QY 265 CAGAGGGGCAACAGAAAGCAGAGGGAGCTCAGAGCGTGAAGATGTTGAAGAG 324
241 CAGAGGGGCAACAGAAAGCAGAGGGAGCTCAGAGCGTGAAGATGTTGAAGAG 300
QY 325 AAGCTGAAGAAAGAGTGTCTCAATTTGTGATATTTGATGATGATGATGATGATG 384
301 AAGCTGAAGAAAGAGTGTCTCAATTTGTGATATTTGATGATGATGATGATGATG 360
QY 385 AAGCCCTCAGAGTCCAGAAATCTGCTACAAAGATGATCTTGTATCAAAACCCGGAATATCT 444
361 AAGCCCTCAGAGTCCAGAAATCTGCTACAAAGATGATCTTGTATCAAAACCCGGAATATCT 420
QY 445 TTGCTGAGATGCTAGTGGCAGACAGATTTACAGATTTAGATGATGCTGTAAATGGGT 504
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781 AATTATTGCTGAGATGAAACATATTA 808

RESULT 14
AB091054 725 bp mRNA linear PRI 11-DEC-2003
LOCUS Homo sapiens mRNA for TICAM-2, complete cds.
DEFINITION
ACCESSION AB091054
VERSION AB091054.1 GI:37360705
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Oshiumi, H., Sasaki, M., Shida, K., Fujita, T., Matsumoto, M. and Seya, T.
TITLE TIR-containing Adapter Molecule (TICAM)-2, a Bridging Adapter
Recruiting to Toll-like Receptor 4 TICAM-1 That Induces
Interferon-{beta}
JOURNAL J. Biol. Chem. 278 (50), 49751-49762 (2003)

PUBMED 14519765
 REFERENCE 2 (bases 1 to 725)
 AUTHORS Oshumi, H., Shida, K., Matsumoto, M. and Seya, T.
 TITLE Direct Submission
 JOURNAL Submitted (28-AUG-2002) Hiroyuki Oshumi, Osaka Medical Center for Cancer and Cardiovascular Diseases, Department of Immunology, 1-3-3 Nakamichi, Higashinari-Ku, Osaka, Osaka 537-0025, Japan
 (E-mail: oshumi@bio.sci.osaka-u.ac.jp, Tel: 81-6-6973-1209, Fax: 81-6-6973-1209)
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 Best Local Similarity 100.0%; Pred. No. 6.7e-139;
 Matches 725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Oy 168 AGGCAGCTGTGATGATCAAGTCCAGGATATCATGAGTTCAGAAAGCTGAAGT 227
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 Oy 228 CTATCTCTGTGATATGTTGCTGAGCAGCAGCATATACAGAGGGGCCAAGAAAGCAG 287
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 Oy 288 GAGGAGCTCAGAGCGTGGAAAGAGATGTTTGAAGAAGAGCTGAAGAGAGGTCTCTC 347
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Oy 708 CGTGATTTCTTACACAGATGAAAGATTTTTCAGAGTCTGTGTATAGACACACAA 767
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 Db 721 TATATA 725
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 ACCESSION AY232653
 VERSION AY232653.1 GI:29470172
 KEYWORDS cds.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 708)
 REFERENCE Fitzgerald, K.A., Rowe, D.C., Barnes, B.J., Caffrey, D.R., Vasinclin, A., Latz, B., Monks, B., Pitha, P.M. and Goldenbock, D.T.
 LPS-TLR4 Signaling to IRF-3/7 and NF- κ B Involves the Toll Adapters TRAM and TRIF
 J. Exp. Med. 198 (7), 1043-1055 (2003)
 14517278
 Oy 2 (bases 1 to 708)
 Db 2 (bases 1 to 708)
 REFERENCE Fitzgerald, K.A., Rowe, D., Barnes, B., Caffrey, D.R., Latz, B., Monks, B., Pitha, P. and Goldenbock, D.T.
 TRIF and TRAM: TLR adapter molecules regulating distinct pathways to IRF-3
 J. Exp. Med. 198 (7), 1043-1055 (2003)
 14517278
 JOURNAL Unpublished
 3 (bases 1 to 708)
 REFERENCE Fitzgerald, K.A., Rowe, D., Barnes, B., Caffrey, D.R., Latz, B., Monks, B., Pitha, P. and Goldenbock, D.T.
 Direct Submission
 TITLE Submitted (09-FEB-2003) Infectious Disease & Immunology, University of Massachusetts Medical School, 366, Plantation Street, Lazare Research Building, Worcester, MA 01605, USA
 JOURNAL
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 Best Local Similarity 100.0%; Pred. No. 2.2e-135; Indels 0; Gaps 0;
 Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: September 23, 2005, 01:29:31 ; Search time 8585 Seconds
(without alignments)
12046.665 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_hic.*
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6: gb_est5.*
7: gb_est6.*
8: gb_gest1.*
9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	733.2	27.0	1005 5	BX391740 BX391740
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4	727.4	26.8	753 7	CR737757 CR737757
5	715.4	26.3	728 6	CB529150 UI-H-FT2
6	707.4	26.0	710 5	BX112907 BX112907
7	663	24.4	681 6	CA440665 UI-H-ED0
8	662	24.4	707 6	CA438249 UI-H-DT1
9	648.2	23.9	887 5	BQ438847 AGENCOURT
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13	567.8	20.9	585 6	CD638761 AGENCOURT
14	554.8	20.4	560 8	AQ319961 RPT11-11
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19	500.4	18.4	1055 1	AL551432 AL551432
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24	461.8	17.0	469 1	AI218114 qh27b07.x

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C 42	308	11.3	501 7	CK980127	CK980127	4111845.B
C 43	287.2	10.6	604 6	CD536283	CD536283	LeukO6.4
C 44	277.4	10.2	740 9	AG515372	AG515372	Mus muscu
C 45	274.8	10.1	525 2	BF286065	BF286065	EST450656

ALIGNMENTS

RESULT 1
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LOCUS BX391704 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
DEFINITION clone CSOD1030YG11 3-PRIME, mRNA sequence.
ACCESSION BX391704
VERSION BX391704.2 GI:46875240
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30619511.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2860.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0BA1020ZG05_CS01863_1ac=2860.r

FEATURES

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/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

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Best Local Similarity 97.7%; Pred. No. 3.6e-15;
Matches 874; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

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 clone CS0D1030YG11 3-PRIME, mRNA sequence.
 ACCESSION BX397140
 VERSION BX397140.2 GI:46846453
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1005)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 13, 2003 this sequence version replaced gi:30613315.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 2860.x
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna78=CS0D1030XD06NP16c=2860.r.
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 DB 756 AAAGCCCTTGGGATCATGAGACTTGTAGTCTCAATTTCTGCCACTGAGATGAA 697
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 QY 2227 CATTAACCTTAAGTACAGAAAAAATATATCATGCTTACAGGCTTTCTTAATAA 2286

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Db	336	ACGGGGAATAGSCCCKACACAGKACCGGGATCCGGACACACGSGKTTTGGCRGKTAACCTTTCA	277
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Db	156	GKTCGTAGTAKRGCTTACGACGCACTTCTCTTKTCAAGNGCANAAANAANNCATTG	97
Oy	2587	TTTGGCCATANTGCTTCTCTGTAAGCCAAATTTTAAATCTAATATAAATGAATGACGCCA	2646
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RESULT 3	CD518425	923 bp	mRNA	linear	EST 06-JUN-2003
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REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
JOURNAL	1 (bases 1 to 923)				
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .				
	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Daniela S. Gerhard, Ph.D.				
	Office of Cancer Genomics				
	National Cancer Institute / NIH				
	Bldg. 31 Rm10A07 Bethesda, MD 20892				
	Email: csgrahbs-remail.nih.gov				
	Tissue Procurement: Dr. Michael Brownstein				
	cDNA Library Preparation: Invitrogen Corp				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNLN at:				
	http://image.llnl.gov				
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Query Match	26.9%	Score 731.2;	DB 6;	Length 923;
Best Local Similarity	94.9%	Pred. No. 1.7e-159;		
Matches 822;	Conservative 0;	Mismatches 33;	Indels 11;	Gaps 6

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Db	681	GAGACTTGTGTCTAGTCCCAATTTCTGCCACTGAGAGTAATGTAACTGTGGGGCAAACTA	740
QY	2006	TTTA-CCCTCTTTATCTGTGAATGAAGGGTT--GAATTGATGCACTCTTAAAGGCT	206
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	CR737757	753 bp	mRNA	linear	EST 27-AUG-2004
LOCUS	CR737757	Soares Placenta Nb2Hp Homo sapiens cDNA clone IMAGE971D037			
DEFINITION	CR737757 Soares Placenta Nb2Hp Homo sapiens cDNA clone IMAGE971D037				
ACCESSION	CR737757				
VERSION	IMAGEL:132835 S [*] , mRNA sequence.				
KEYWORDS	CR737757.1 GI:51587215				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
TITLE	I (bases 1 to 753)				
JOURNAL	Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E., Peters,M., Radelof,U. and Schneider,D. I.M.A.G.E. cDNA Clone Collection Unpublished (2004)				
COMMENT	Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Email: www.rzpd.de RZPD; IMAGP971D037. RZPDLIB: I.M.A.G.E. cDNA clone collection; Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel.: +49 30 32639 100 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAACAAGCTATGAC. Location/Qualifiers 1..753 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGP971D037 , IMAGR:132835" /bes="female" /dev_stage="placenta obtained at birth (full term)" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares placenta Nb2HP" /note="Organ: placenta; Vector: pUT3J (pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACGGAGAATTGC GGCGCCGACGAAATTTT TTTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. library constructed by Bento Soares and M.Patima Bonaldo."				
FEATURES	Source				
	Query Match	26.8%; Score 727.4;	DB 7;	Length 753;	
	Best Local Similarity	99.6%;	Pred. No. 1.3e-158;		
	Matches 750;	Conservative 0;	Mismatches 1;	Indels 2;	Gaps 2;
ORIGIN					
Dy	1206 AGGAGATTGTGATCACACTTCTCCTCCGAGGCACTTCATGTGTAATTAAGCATTCG	1265			
Dd	1 AGGAGANTTGATGACACACTTCTCCTCCGAGGCACTTCATGTGTAATTAAGCATTCG	60			
Oy	1266 GGTACTATACCACCGAATAATGAAATGGCAGAAATGAACATTTAGCATGTAAAGCGTTGA	1325			
Dd	61 GTTACTATACCACCGAATAATGAAATGGCAGAAATGAACATTTAGCATGTAAAGCGTTGA	120			
Oy	1326 TGCAATATAAATCAGAAAATAGATGTGAGATGTGTGAACTTTTAAAGAACCCAGTCAA	1385			
Dd	121 TGCAATATAAATCAGAAAATAGATGTGAGAAATGTGTGAACTTTTAAAGAACCCAGTCAA	180			
Oy	1386 ATGATATTTTTCGCTGAAATTCGCATATTTTGGAGGCAATTTCCACACCGATTCACAGCCC	1445			
Dd	181 ATGATATTTTTCGCTGAAATTCGCATATTTTGGAGGCAATTTCCACACCGATTCACAGCCC	240			
Oy	1446 ATTGATATGTGTGATTAAGGACCTTCGTGAGATGTGTTCACAGCGTCCCCCTGGGGCTT	1505			

Db	241	ATTGATAGTGTAGTATAGGACCTCGTGAATGGTTCAGACGTCCCTGGGGCTT	300
Qy	1506	AAATCTCTTCATATTAGTCATCATTTTGTAACTAATGGCTTATTTGGACAAGCTTCTAAAG	1566
Db	301	AAATCTCTTCATATTAGTCATCATTTTGTAACTAATGGCTTATTTGGACAAGCTTCTAAAG	360
Qy	1566	GGCATTAACGTGTGAGTGGCCAGATATATCACTTTTATGATCAAAAACCTCTTATGGA	1626
Db	361	GGCATTAACGTGTGAGTGGCCAGATATATCACTTTTATGATCAAAAACCTCTTATGGA	420
Qy	1626	AGCTTTAAAAGTTTCCGTCAACAACAATTCCTTCTCGAAGATATTTCTCATTTAGGTC	1686
Db	421	AGCTTTAAAAGTTTCCGTCAACAACAATTCCTTCTCGAAGATATTTCTCATTTAGGTC	480
Qy	1686	TTCAAAGTAGCCTACCTGTGTGCAATGTGTGTGTGTATAGTTATTTATTAAGAATTGG	1746
Db	481	TTCAAAGTAGCCTACCTGTGTGCAATGTGTGTGTGTATAGTTATTTATTAAGAATTGG	540
Qy	1746	ATAGAGAGATGTATTTTATTAACCTCTATTTAGAGCCCAATGCTCTAAACAAGCAG	1806
Db	541	ATAGAGAGATGTATTTTATTAACCTCTATTTAGAGCCCAATGCTCTAAACAAGCAG	600
Qy	1806	AGAGGCCCAACA - GGAATGTGTTCTTTCCTCCACAGCCCTTGTGCCATGTGAGATTGA	1866
Db	601	AGAGGCCCAACAAGGATGTGTTCTTTCCTCCACAGCCCTTGTGCCATGTGAGATTGA	660
Qy	1866	GGAGGCAATCGTCCACTTGAGATCAAGGATGGGGTGGAGAA - GGGTCAATGTCACTAATG	1926
Db	661	GGAGGCAATCGTCCACTTGAGATCAAGGATGGGGTGGAGAAATGGGTCATGTCAATGTAATG	720
Qy	1924	AGAAAGACCCCTCTGGGATCATGAGACTTGGT	1956
Db	721	AGAAAGACCCCTCTGGGATCATGAGACTTGGT	753

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RESULT 5
CB529150/c
LOCUS CB529150 728 bp mRNA linear EST 05-AUG-2000
DEFINITION UI-H-PT2-bJf-a-01-0-UI.g1 NCI_CGAP_F12 Homo sapiens cDNA clone
ACCESSION CB529150
VERSION CB529150
KEYWORDS CB529150.1 GI:29389547
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 728)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq Primer: M13 FORWARD
POLYA=yes.
location/Qualifiers
1..728
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-PT2-bJf-a-01-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI_CGAP_F12"

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/note="Organ: Lung; Vector: pPT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP P72 is a subcloned cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours; PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-P72
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 26.3%; Score 715.4; DB 6; Length 728;
Best Local Similarity 99.9%; Pred. No. 8.1e-156;
Matches 716; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 219 TCTGAAGTATCTATCTTGTGTAATGCTGAGCAGCAATATCAACAGAGGGCCAA 278
Db 728 TCTGAAGTATCTATCTTGTGTAATGCTGAGCAGCAATATCAACAGAGGGCCAA 669
Oy 279 GGAAGAGAGAGAGAGCTCAGAGCCTGAGAGATGTTTGAAGAAGAGCTGAAGA 338
Db 668 GGAAGAGAGAGAGAGCTCAGAGCCTGAGAGATGTTTGAAGAAGAGCTGAAGA 609
Oy 339 GTGTTCTCAATTTGTGATATGTCATGACAGAGATGACAGATGAAGCCCTCAG 398
Db 608 GTGTTCTCAATTTGTGATATGTCATGACAGAGATGACAGATGAAGCCCTCAG 549
Oy 399 CAGATCGCTCAAGATGATGCTTGTGATCAACCCGGAATATCTTGTGAGATGCC 458
Db 548 CAGATCGCTCAAGATGATGCTTGTGATCAACCCGGAATATCTTGTGAGATGCC 489
Oy 459 TGTGGCAGACAGATTTACAGAAATTTAGATGCTGTAATGGGTCTGATGACAATC 518
Db 488 TGTGGCAGACAGATTTACAGAAATTTAGATGCTGTAATGGGTCTGATGACAATC 429
Oy 519 TTATTACTGACTGAATTTTAAAGATCTTGTTAAATTTCCAGTTCTATACGTC 578
Db 428 TTATTACTGACTGAATTTTAAAGATCTTGTTAAATTTCCAGTTCTATACGTC 369
Oy 579 CTATGAATCTCCGTTACAGGACGATTAATCAACTCTGTTATACCATCCGCCCC 638
Db 368 CTATGAATCTCCGTTACAGGACGATTAATCAACTCTGTTATACCATCCGCCCC 309
Oy 639 AACATGCCCCCTCCGGAAGAAGACTCCCTTGGCCCTCAACCATCAATGCTTGA 698
Db 308 AACATGCCCCCTCCGGAAGAAGACTCCCTTGGCCCTCAACCATCAATGCTTGA 249
Oy 699 GAAAGAAAGTCTGATTTCTTACACAGTAAAGAAATTTTTCAGAGTCTGTATPAG 758
Db 248 GAAAGAAAGTCTGATTTCTTACACAGTAAAGAAATTTTTCAGAGTCTGTATPAG 189
Oy 759 ACAACAACAATATATGAGAAAGAGACAAGAAATATGATCAACAAGCAATTAATG 818
Db 188 ACAACAACAATATATGAGAAAGAGACAAGAAATATGATCAACAAGCAATTAATG 129

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Oy 819 GATGAACATATTAACATATGCTGCTGCTTTGTTGTAACCAATGATTAATCTTCA 878
Db 128 GATGAACATATTAACATATGCTGCTGCTTTGTTGTAACCAATGATTAATCTTCA 69
Oy 879 TGAGAAAGCAGTTCTTGAAGAAATGTTTAAATTAAGAGAGCTTCACTTAAGAA 935
Db 68 TGAGAAAGCAGTTCTTGAAGAAATGTTTAAATTAAGAGAGCTTCACTTAAGAA 12

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RESULT 6

EX112907 710 bp mRNA linear EST 07-FEB-2003
LOCUS EX112907 Soares fetal liver spleen INF15 Homo sapiens cDNA clone
DEFINITION IMAG9809130 ; IMAGE:127472, mRNA sequence.

ACCESSION EX112907
VERSION EX112907.1 GI:27837927
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 710)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Patsch,B., Peters,M., Radehof,U., Schneider,D. and Korn,B.
Homo sapiens
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfe
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAG9809130.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfe
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

COMMENT

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M31r, primer sequence: TTTCACACAGAAACAGCTATGAC.
Location/Qualifiers
1. 710
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAG9809130 ; IMAGE:127472"
/sex="male"
/dev stage="20 week-post conception fetus"
/lab host="DH10B (ampicillin resistant)"
/clone.lib="Soares fetal liver spleen INF15"
/note="Organ: Liver and Spleen; Vector: pPT73D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAACAATTAATTAAGAATCTTTTATTTTATTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pPT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

FEATURES

source

ORIGIN

Query Match 26.0%; Score 707.4; DB 5; Length 710;
Best Local Similarity 99.7%; Pred. No. 5.9e-154;
Matches 708; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 1728 TATTTAATGAAGCTTTGATAGAGAGATGATTTTATTAATCTCTATTTAGAGCCC 1787
Db 1 TATTTAATGAAGCTTTGATAGAGAGATGATTTTATTAATCTCTATTTAGAGCCC 60
Oy 1788 ATGCTCTTAACAGCCAGAGAGCCCAACAGAGATTTTCTTCTCCACAGCCCTTC 1847

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Db      61 ATGCTCTTAACAAGCCAGAGAGGCCCCAAACAGATGTTGTTCTTCTCCACAGCCCTTC 120
Qy      1848 TGGCCCATCGAATTGAGGAGAGATGTCCTCACTTGATCAGAGAGAGGAGAAATG 1907
Db      121 TGGCCCATCGAATTGAGGAGAGATGTCCTCACTTGATCAGAGAGAGGAGAAATG 180
Qy      1908 GTCATGTCATGTAATGAGAAAGCCCTCTCCGGATCATGAGACTTGTTCTAGTCCAA 1967
Db      181 GTCATGTCATGTAATGAGAAAGCCCTCTCCGGATCATGAGACTTGTTCTAGTCCAA 240
Qy      1968 TTCTGCGCACTGAGATGAAATGTAAGTGTGGGCAAACTATTACCTCTCTTATCTGTGA 2027
Db      241 TTCTGCGCACTGAGATGAAATGTAAGTGTGGGCAAACTATTACCTCTCTTATCTGTGA 300
Qy      2028 ATGAAAGGGTGAATGATGAGATCTCTAAAGGCTTTGCTCTATGAGAGATGTAAGAA 2087
Db      301 ATGAAAGGGTGAATGATGAGATCTCTAAAGGCTTTGCTCTATGAGAGATGTAAGAA 360
Qy      2088 CTAGGAGCCACAAAGAGAAACAAGCAAAAGTTTGGATTGATAAGTATATATAT 2147
Db      361 CTAGGAGCCACAAAGAGAAACAAGCAAAAGTTTGGATTGATAAGTATATATATAT 420
Qy      2148 GTTGCAGAAAGGCTTTATATATGCTTATATATGAAAAATATTTTGTATATGACAGAT 2207
Db      421 GTTGCAGAAAGGCTTTATATATGCTTATATATGAAAAATATTTTGTATATGACAGAT 480
Qy      2208 AATTTATTTTAAATGCTGTCATTAACCTTAAGTCAAGAAAAAAATATATACCTTAC 2267
Db      481 AATTTATTTTAAATGCTGTCATTAACCTTAAGTCAAGAAAAAAATATATACCTTAC 540
Qy      2268 TCAGGCTTCTTAAATAATATTTTATAGAGATCTTGTAGTAAGACATTTTGCTTAAT 2327
Db      541 TCAGGCTTCTTAAATAATATTTTATAGAGATCTTGTAGTAAGACATTTTGCTTAAT 600
Qy      2328 TTCTTTTCTTATTTCCCACTTGTATATCCCTTACAGTACCGGATGTGACACATCT 2387
Db      601 TTCTTTTCTTATTTCCCACTTGTATATCCCTTACAGTACCGGATGTGACACATCT 660
Qy      2388 TTTTGCAGTACCTCTTCAATGACATGAACAACAGTTCTATGAGAGAT 2437
Db      661 TTTTGCAGTACCTCTTCAATGACATGAACAACAGTTCTATGAGAGAT 710

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RESULT 7
CA440665/c      681 bp      mRNA      linear      EST 08-NOV-2002
LOCUS      CA440665      UI-H-ED0-axc-b-08-0-UI.s1 NCI CGAP EDO Homo sapiens cDNA clone
DEFINITION      UI-H-ED0-axc-b-08-0-UI 3', mRNA sequence.
ACCESSION      CA440665
VERSION        CA440665.1 GI:24805085
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1 (bases 1 to 681)
AUTHORS      NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaab-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuend
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-47, >AT richLow_complexity (matched complement)
Seq primer: M13 FORWARD
POLY(A)=yes.
Location/Qualifiers

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source
1..681
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-ED0-axc-b-08-0-UI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI CGAP EDO"
/note="Organ: Left Pubic Bone; Vector: pRT3-Pac
(Pharmacia) with a modified polylinker; Site 1: BcoR I;
Site 2: Not I; NCI CGAP EDO is a cDNA library containing
the following tissue(s): Chondrosarcoma cell line C55. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an BcoR I adaptor, digested with Not I, and cloned
directionally into pRT3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dr)18 tail. The sequence tag for this
library is GCTCAAGCT.
TAG_RISUB=chondrosarcoma
TAG_LIB=UI-H-ED0
TAG_SEQ=CTCAAGCT"

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ORIGIN
Query Match      24.4%; Score 663; DB 6; Length 681;
Best Local Similarity 100.0%; Pred. No. 1,4e-143;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2055 AAGGCTTTTGTCCCTATGAGATGTGAAAACTAGGAGCAACAAGAGAAACAA 2114
Db      681 AAGGCTTTTGTCCCTATGAGATGTGAAAACTAGGAGCAACAAGAGAAACAA 622
Qy      2115 AAAAGTTGATTCGATTAAGTATAGTAATAGTTGAGAAAGCTTTATATAGCTTAT 2174
Db      621 AAAAGTTGATTCGATTAAGTATAGTAATAGTTGAGAAAGCTTTATATAGCTTAT 562
Qy      2175 AATGAAAGATTTTGTATATGATGACAGATATATTTTAAATGCTGATTAAC 2234
Db      561 AATGAAAGATTTTGTATATGATGACAGATATATTTTAAATGCTGATTAAC 502
Qy      2235 TTAAGTCACAGAAAAATATACATGCTTACTAGGCTTCTTAAATAATTTTAA 2294
Db      501 TTAAGTCACAGAAAAATATACATGCTTACTAGGCTTCTTAAATAATTTTAA 442
Qy      2295 TAGAGATCTTGTAGTAAGACATTTTGCTTAATTTCTTTTCTTATTTCCCACTTGAT 2354
Db      441 TAGAGATCTTGTAGTAAGACATTTTGCTTAATTTCTTTTCTTATTTCCCACTTGAT 382
Qy      2355 ATCCCTACAGTACCGGGATCTGACACATTTTTCAGATTAACCTGATACAGCAG 2414
Db      381 ATCCCTACAGTACCGGGATCTGACACATTTTTCAGATTAACCTGATACAGCAG 322
Qy      2415 AACCAAAAGCTTCTATGAGAGATGCAAGTAAGTCAAGCTCTTATCTGTAGTACT 2474
Db      321 AACCAAAAGCTTCTATGAGAGATGCAAGTAAGTCAAGCTCTTATCTGTAGTACT 262
Qy      2475 ATTAGAGAGAGATGTTTTCATTTGATGATGACATTTTCTTACCTTAAAGTTCTGAT 2534
Db      261 ATTAGAGAGAGATGTTTTCATTTGATGATGACATTTTCTTACCTTAAAGTTCTGAT 202
Qy      2535 AGTAGCTTACTACTACTCTCTTTTTCAGTTTTCATATATAGTATCATTTTGTGCA 2594
Db      201 AGTAGCTTACTACTACTCTCTTTTTCAGTTTTCATATATAGTATCATTTTGTGCA 142
Qy      2595 TAATGCTTCTGTAAAGCAATTTTATATATATATATATATATATATATATATATAT 2654
Db      141 TAATGCTTCTGTAAAGCAATTTTATATATATATATATATATATATATATATATAT 82
Qy      2655 GCTGCGCAAACTTGAGGAGATGATGCTAAATGATTTTAAATAATGTTTATATTC 2714

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Db		81 GCCTGCCAAACTGGGCGCATTTGAATGCCTTAAGTATTCTTTAATAAATGTTTTATTC	22
Oy	2715 TTT 2717 		
Db	21 TTT 19		
RESULT 8			
LOCUS	CA438249/c	707 bp mRNA linear EST 08-NOV-2002	
DEFINITION	UI-H-DT1- <i>bw-e-13-0-UI</i> .s1 NCI CGAP DT1 Homo sapiens cDNA clone		
VERSION	UI-H-DT1- <i>bw-e-13-0-UI</i> 3', mRNA sequence.		
ACCESSION	CA438249		
KEYWORDS	CA438249.1 GI:24802669		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 707)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Jose Mercende cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA library arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu The following repetitive elements were found in this cDNA sequence: 1-47, >AT rich#Low_complexity (matched complement) Seq primer: M13 FORWARD POLYA=yes.		
FEATURES	Location/Qualifiers		
SOURCE	1..707		
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	/db_xref="taxon:9606"		
	/clone="UT-H-DT1- <i>bw-e-13-0-UI</i> "		
	/tissue_type="Metastatic Chondrosarcoma"		
	/dev_stage="Adult"		
	/lab_host="DH10B (Life Technologies)"		
	/clone_lib="NCI_CGAP DT1"		
	/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP DT1 is a normalized cDNA library containing the following tissue(s): Metastatic Chondrosarcoma in lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTTCGG." TAG_TISUE=lung metastatic chondrosarcoma TAG_LIB=UI-H-DT1 TAG_SEQ=AACTGTTCGG"		
ORIGIN			
	Query Match 24.4%; Score 662; DB 6; Length 707; Best Local Similarity 99.1%; Pred. No. 2.3e-143; Matches 676; Conservative 0; Mismatches 5; Indels 1; Gaps 1;		
Oy	2036 GTTGAAATGATGAGATCTCTAAAGGCTTTTGCCCTTAGAGAGATGTAAGAAAATCAGGAC	2055	
Db	699 GGTTGAATGATGAGATCTCTAAAGG- TTGTGCTCTTAAGAGATGTGA AAAAATCAGGAC	641	

Accession	Version	Keywords	Organism	Reference	Authors	Journal	Comment
2096							
2096							
640							
2156							
580							
2216							
520							
2216							
460							
2336							
400							
2396							
340							
2456							
280							
2516							
220							
2576							
160							
2636							
100							
2696							
40							
RESULT 9							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
ORGANISM							
REFERENCE							
AUTHORS							
JOURNAL							
COMMENT							

FEATURES

Location/Qualifiers
1..887
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6018003"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIM MGC 70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 Kb. Library constructed by life technologies."

ORIGIN

Query Match 23.9%; Score 648.2; DB 5; Length 887;
Best Local Similarity 95.2%; Pred. No. 4,1e-140;
Matches 698; Conservative 0; Mismatches 32; Indels 3; Gaps 3;

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Qy 42 TCGCTGCGATTGAAAAGAAATGCTGAAATATACATAAAGTTTCTCTTCTGCTTGG 101
Db 146 TGGCCTATTGATGAAAAGAAATGCTGAAATATACATAAAGTTTCTCTTCTGCTTGG 205
Qy 102 ATATTATATATGGGATGCGGAAGTCTTAAATTAATTCCTGCTCTTCTCTCTTGG 161
Db 206 ATATTATATATGGGATGCGGAAGTCTTAAATTAATTCCTGCTCTTCTCTCTTGG 265
Qy 162 GGTAAAGGACAGTGTGGATACAGTCCAGGATATCATGAGTCAGATTCAGAAAGTCT 221
Db 266 GGTAAAGGACAGTGTGGATACAGTCCAGGATATCATGAGTCAGATTCAGAAAGTCT 325
Qy 222 GAAGATCTATCTTGTATATGTTGCTGAGCAGACAAATACAAAGAGGGCCACAGAA 281
Db 326 GAAGATCTATCTTGTATATGTTGCTGAGCAGACAAATACAAAGAGGGCCACAGAA 385
Qy 282 AAGCAGAGGAGCTCAAGAGCTGGAAGAGATGTTTGAAGAAAGCTGGAAGAAAGTGT 341
Db 386 AAGCAGAGGAGCTCAAGAGCTGGAAGAGATGTTTGAAGAAAGCTGGAAGAAAGTGT 445
Qy 342 TTCCTCAATTTGTATATGATGATGACAGAAATGACAGATGAAGCCCTCAGATCCAG 401
Db 446 TTCCTCAATTTGTATATGATGATGACAGAAATGACAGATGAAGCCCTCAGATCCAG 505
Qy 402 AATCTGTACAAAGATGATCTTGTATCAAAACCCGGAATATCTTTGCTGAGATGCATGT 461
Db 506 AATCTGTACAAAGATGATCTTGTATCAAAACCCGGAATATCTTTGCTGAGATGCATGT 565
Qy 462 GGCAGACAGCATTTACAGATTTAGATGATGCTGTAATGGGTCTGCAATGCAATCTTA 521
Db 566 GGCAGACAGCATTTACAGATTTAGATGATGCTGTAATGGGTCTGCAATGCAATCTTA 625
Qy 522 TTACTGATCGAAAACCTTTTAAAGATCTTGTGTAATTTCCAGTCTATACGCTCCTA 581
Db 626 TTACTGATCGAAAACCTTTTAAAGATCTTGTGTAATTTCCAGTCTATACGCTCCTA 685
Qy 582 ATGAATCTCGTTTAAAGAGCAGATTAATCAACTGTATTATCCATGCGGCCCTGAAC 641
Db 686 ATGAATCTCGTTTAAAGAGCAGATTAATCAACTGTATTATCCATGCGGCCCTGAAC 745
Qy 642 AATCCCTCTTCCCGAAGAAAGACT-CCCTTGGCCCTCCAAACATCAATG-CTTTAGAG 699
Db 746 AATCCCTCTTCCCGAAGAAAGACTCCCTTGGCCCTCCAAACATCAATGCTTTAAAG 805
Qy 700 AAGAAAGTGTG-AGATTCTCTACAGAGTGAAGAAATTTTCAGAGTCTGTATAAG 758
Db 806 AAGAAAGTGTGAGATTCTCTACAGAGTGAAGAAATTTTCAGAGTCTGTATAAG 865
Qy 759 ACACAAACAACCTA 771
Db 866 AAGACACACNACAA 878

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RESULT 10

CA441688/c

LOCUS CA441688 635 bp mRNA linear EST 08-NOV-2002
DEFINITION UI-H-ED0-ax1-a-05-0-UI.s1 NCI CGAP ED0 Homo sapiens CDNA clone
UI-H-ED0-ax1-a-05-0-UI 3', mRNA sequence.
ACCESSION CA441688
VERSION CA441688.1 GI:24806108
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 635)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

TUMOR

Unpublished (1997)
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-remail.nih.gov

COMMENT

Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this CDNA
sequence: 1-54, >AT rich#low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers
1..635
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-ED0-ax1-a-05-0-UI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP ED0"
/note="Organ: Left Pubic Bone; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP ED0 is a CDNA library containing the following tissue(s): Chondrosarcoma cell line C55. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGCT.
TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-ED0
TAG_SEQ=GCTCAAGCT"

ORIGIN

Query Match 22.5%; Score 610; DB 6; Length 635;
Best Local Similarity 100.0%; Pred. No. 3.1e-131;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2108 CAAGCAAAAAGTTGATTCGATTAAGTATATGTAATAGTTCGCAAGAGCTTTATATA 2167
Db 635 CAAGCAAAAAGTTGATTCGATTAAGTATATGTAATAGTTCGCAAGAGCTTTATATA 576
Qy 2168 TGCCTATATATGAAAAGATATTTTGTATATGACAGCATATTAATTTTAAATCTGTC 2227
Db 575 TGCCTATATATGAAAAGATATTTTGTATATGACAGCATATTAATTTTAAATCTGTC 516
Qy 2228 ATTACACTTAAAGTCACAGAAAAAATATATCATGCTTACTCAGGCTTTCTTAAATATA 2287
Db 515 ATTACACTTAAAGTCACAGAAAAAATATATCATGCTTACTCAGGCTTTCTTAAATATA 456

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QY	2288	ATTTTTATAGAGATCTCTGAGTAAAGACATTTGGTTAATTTCTTTTCTTATCCGCA	2347
Db	485	ATTTTATAGAGATCTCTGAGTAAAGACATTTTGGTTAATTTCTTTTCTTATCCGCA	396
QY	2348	CTTGTAATATCCCTTACCAATACCGGAGATCTGCACATCTTTTTCAGTTACCTCTTCAT	2407
Db	395	CTTGTAATATCCCTTACCAAGTACCGGAGATCTGCACATCTTTTTCAGTTACCTCTTCAT	336
QY	2408	AGGCATGAACCAAACGTTCTTATGAGAGACATGCAAGTAAAGCAAGCCTCCATATCCGTT	2467
Db	335	AGGCATGAACCAAACGTTCTTATGAGAGACATGCAAGTAAAGCAAGCCTCCATATCCGTT	276
QY	2468	AGTACTTATTAGAGAGAGAGATGTTTTTCATATGCATATGACATTTCTTACGCTTAAAG	2527
Db	275	AGTACTTATTAGAGAGAGAGATGTTTTTCATATGCATATGACATTTCTTACGCTTAAAG	216
QY	2528	TTTCTGATAGTACCTTACTACTGACTTCTCTCTTTTCAGTTTTCTATTAATAGTATCATTTT	2587
Db	215	TTTCTGATAGTACCTTACTACTGACTTCTCTCTTTTCAGTTTTCTATTAATAGTATCATTTT	156
QY	2588	TTTGGCATTAATAGCTTCCGTAAAGCCAAATTTTATATCAATTAATAAACAAGTACGCCAC	2647
Db	155	TTTGGCATTAATAGCTTCCGTAAAGCCAAATTTTATATCAATTAATAAACAAGTACGCCAC	96
QY	2648	TCTTCATGCTCGCCAAACTTGGGGCAATTGAATGCTAAATGGTATTTTAAATAAATGTT	2707
Db	95	TCTTCATGCTCGCCAAACTTGGGGCAATTGAATGCTAAATGGTATTTTAAATAAATGTT	36
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Db	35	TTTATATCTTT 26	

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/clone="IMAGE:2540746"
/clone_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_1ib="Morton Fetal Cochlea"
/notes="Organ: ear; Vector: pBluescript SK-; Site: 1: EcoRI Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: Oligo dt. Fetal cochlea, normal 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton -5' adaptor sequence: 5' GAATTCGACACAG 3' -3' adaptor sequence: 5' CTCGACGTTTTTTTTTTTTTTTTT 3'"

```

RESULT	11	
LOCUS	BI493312	
DEFINITION	BI493312 615 bp mRNA linear EST 28-AUG-2001	
ACCESSION	D59966.12	Morton Fetal Cochlea Homo sapiens cDNA clone
VERSION	BI493312	IMAGE:2540746 5', mRNA sequence.
KEYWORDS	BI493312.1	GI:15332656
SOURCE	EST.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 615)	
TITLE	Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.	
JOURNAL	Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening	
MEDLINE	Genomics 23, 42-50 (1994)	
PUBMED	9513011	
COMMENT	7829101	
	Contact: Morton, C. C.	
	Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology	
	Brigham and Women's Hospital	
	75 Francis Street, Harvard Medical School, Boston, MA 02115, USA	
	Tel: 617 732 7980	
	Fax: 617 738 6996	
	Email: cmorton@rics.bwh.harvard.edu	
	DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).	
	This clone is available royalty-free through LMLT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	
	Plate: LHM6328 row: N column: 11	
	Seq primer: M13RPL reverse primer (ABI).	
FEATURES	Location/Qualifiers	
SOURCE	1..615	
	organism="Homo sapiens"	
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	/db_xref="taxon:9606"	

Query Match	22.3%	Score 606.4	DB 4	Length 615
Best Local Similarity	99.8%	Pred. No. 2.2e-130		
Matches 607	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy	2098	CAAAAGGGAACAAACAAAAAGTTTGATTCGATTAAGTGAATGATATGATATAGTTCAGAG	2157	
Db	8	CAAAAGGGAACAAACAAAAAGTTTGATTCGATTAAGTGAATGATATGATATAGTTCAGAG	67	
Qy	2158	GCTTTATATATGCTTATATATGAAAAAGATTTTTTGTATATATGACAGATATTTATTTT	2211	
Db	68	GCTTTATATATGCTTATATATGAAAAAGATTTTTTGTATATATGACAGATATTTATTTT	127	
Qy	2218	TAATGCTGCTATTCACCTTAAGTCACAGGAAAAAATATACATGCTTACAGGCTTTC	2277	
Db	128	TAATGCTGCTATTCACCTTAAGTCACAGGAAAAAATATACATGCTTACAGGCTTTC	187	
Qy	2278	TTAAAAAATAATTTTATTAAGAGATCCTTGAGTAAAGAATTTTGCTTATTTCTTTTTC	2337	
Db	188	TTAAAAAATAATTTTATTAAGAGATCCTTGAGTAAAGAATTTTGCTTATTTCTTTTTC	247	
Qy	2338	TTAATCCCACTTGATATCCCTTACAGATACCGGGATTCGACACATCTTTTGCAGT	2397	
Db	248	TTAATCCCACTTGATATCCCTTACAGATACCGGGATTCGACACATCTTTTGCAGT	307	
Qy	2398	ACCTCTTCATAGCCATGAACCAAAAGCTTCTATGAGAGCATGCAAGTAAGTCAAGCTC	2457	
Db	308	ACCTCTTCATAGCCATGAACCAAAAGCTTCTATGAGAGCATGCAAGTAAGTCAAGCTC	367	
Qy	2458	CTATTCGTGTAGTACTTATTAAGAGAGAGATGGTTTTTCATGATAGTGAATTTTCTT	2517	
Db	368	CTATTCGTGTAGTACTTATTAAGAGAGAGATGGTTTTTCATGATAGTGAATTTTCTT	427	
Qy	2518	AGCCTTAACGTTCTGATAGTAGCTTACTCACTTCTCTTTTCAGTTTCAATAATAG	2577	
Db	428	AGCCTTAACGTTCTGATAGTAGCTTACTCACTTCTCTTTTCAGTTTCAATAATAG	487	
Qy	2578	TATTCATTTTTTTCGCATTAATGCTTCTCTGTAAGGCCAATTTTATATACATAATAACATG	2637	
Db	488	TATTCATTTTTTTCGCATTAATGCTTCTCTGTAAGGCCAATTTTATATACATAATAACCTG	547	
Qy	2638	AACGCGCCACTCTTCATAGCTCGCCAAACTTGGGGCAATTGATGCTAATAGTATTTTTTA	2697	
Db	548	AACGCGCCACTCTTCATAGCTCGCCAAACTTGGGGCAATTGATGCTAATAGTATTTTTTA	607	
Qy	2698	AATAAATG 2705		
Db	608	AATAAATG 615		
RESULT 12	BI493311/c	613 bp	mRNA	linear
LOCUS	d69906.w.1	Morton Fetal Cochlea	Homo sapiens	CDNA clone
DEFINITION	IMAGE:2540746 3', mRNA sequence.			
ACCESSION	BI493311			
VERSION	BI493311.1	GI:15332655		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE 1 (bases 1 to 613)
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 TITLE Robertson, N.G., Kietarapal, U., Gutierrez-Bespeleta, G.A., Biber, P.R., and Morton, C.C.
 JOURNAL Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening
 MEDLINE Genomics 23, 42-50 (1994)
 PUBMED 95130111
 7829101
 COMMENT Contact: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Place: LLM6328 row: N column: 11
 Seq primer: T7 primer.
 Location/Qualifiers
 1..613
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540746"
 /issue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site: 1: EcoRI, Site: 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: Oligo dT. Fetal cochlea, normal. 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton. -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT 3' "

ORIGIN

Query Match 22.2%; Score 602.8; DB 4; Length 613;
 Best Local Similarity 99.7%; Pred. No. 1.5e-129;
 Matches 604; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2098 CAAAAGGAAACAAGGTTGATTCGATTAAGATATGTAATAGTTGAGAAG 2157
 606 CAAAAGGAAACAAGGTTGATTCGATTAAGATATGTAATAGTTGAGAAG 547
 2158 GCTTTATATATGCTTTAATGAAGAATTTTTTGTATATGACGCAATATTATTT 2217
 546 GCTTTATATATGCTTTAATGAAGAATTTTTTGTATATGACGCAATATTATTT 487
 2218 TAATGCTGATTAACCTTAAGTCAAGGAAATATATATGCTTACTGAGGCTTC 2277
 486 TAATGCTGATTAACCTTAAGTCAAGGAAATATATATGCTTACTGAGGCTTC 427
 2278 TTAATAATATATTTTATAGAGATCTTGATTAAGACATTTTGCTTAATTTCTTTTC 2337
 426 TTAATAATATATTTTATAGAGATCTTGATTAAGACATTTTGCTTAATTTCTTTTC 367
 2338 TTAATCCCACTTGTATATCCCTTACGATCCGGATCGACATCTTTTGAAGTT 2397
 366 TTAATCCCACTTGTATATCCCTTACGATCCGGATCGACATCTTTTGAAGTT 307
 2398 ACCCTCTTACGATGAACCAAAAGCTTCTATGAGAGCATGCAAGTAAGCAACCTC 2457
 306 ACCCTCTTACGATGAACCAAAAGCTTCTATGAGAGCATGCAAGTAAGCAACCTC 247
 2458 CTATCTGTAGTACTTATTAAGAGAGAGATGCTTTTCAATGATGACATTTTCTT 2517

RESULT 13
 LOCUS CD638761
 DEFINITION AGENCOURT_14535036 NIH_MGC_191 Homo sapiens cDNA clone
 ACCESSION CD638761
 VERSION CD638761.1 GI:31804901
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 585)
 NIH-MGC http://mhc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10X07 Bethesda, MD 20892
 Email: cgsabbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: NDCM218 row: 1 column: 20
 High quality sequence stop: 548.
 Location/Qualifiers
 1..585
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30417403"
 /issue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 191"
 /note="Vector: pDR-LIB, Site: 1: SfiI (ggcgatcagcgc); Site: 2: SfiI (ggcgctcgcgc); Library is oligo-dT primed and directionally cloned. PMBC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA and Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTAAGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGACGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

246 CTATCTGTAGTACTTATTAAGAGAGAGATGTTTCATTCATGATGACATTTTCTT 187
 2518 AGCTTAACGTTCTGATAGTACTTACTTCTTTTCAGTTTCATATATAG 2577
 186 AGCTTAACGTTCTGATAGTACTTACTTCTTTTCAGTTTCATATATAG 127
 2578 TATGATTTTTTGGCATTAATGCTTCGTAAAGCAATTTATATTAATTAACAG 2637
 126 TATGATTTTTTGGCATTAATGCTTCGTAAAGCAATTTATATTAATTAACAG 67
 2638 AACTGCCACCTTTCATGCTCCGCAACTGGGGCAATTTGATGTAATGTAATTTTAA 2697
 66 AACTGCCACCTTTCATGCTCCGCAACTGGGGCAATTTGATGTAATGTAATTTTAA 7
 2698 AATTA 2703
 6 AATTA 1

Query Match 20.9%; Score 567.8; DB 6; Length 585;
 Best Local Similarity 99.5%; Pred. No. 2.2e-121;
 Matches 580; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1499 GGGGCTTAATCTCTTCAATTAAGTCAATGTTGTAAGCTTTATTTGACAGCTT 1558
 DB 3 GGGGCTTAATCTCTTCAATTAAGTCAATGTTGTAAGCTTTATTTGACAGCTT 62
 QY 1559 CTAAAGGGGTTAACTGTGTGAGTCCAGATATTCATTTTAAATCAAAAACCTTC 1618
 DB 63 CTAAAGGGGTTAACTGTGTGAGTCCAGATATTCATTTTAAATCAAAAACCTTC 122
 QY 1619 TTATGAACTTTAAAGTTTCCGTCAACAAATCTCTTCAGAAAGTATTTCTCAT 1678
 DB 123 TTATGAACTTTAAAGTTTCCGTCAACAAATCTCTTCAGAAAGTATTTCTCAT 182
 QY 1679 TTAGTCTTCAAAAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1738
 DB 183 TTAGTCTTCAAAAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
 QY 1739 ACTTTGATAGAGAGATGATTTTATTAACCTCTTCTAGAGCCCATGCTCTTAC 1798
 DB 243 ACTTTGATAGAGAGATGATTTTATTAACCTCTTCTAGAGCCCATGCTCTTAC 302
 QY 1799 AAGCCAG 1858
 DB 303 AAGCCAG 362
 QY 1859 GATTGAG 1918
 DB 353 GATTGAG 422
 QY 1919 TTAATGAAAG 1978
 DB 423 TTAATGAAAG 482
 QY 1979 AGATGAAATGTAAGTGTGGGCAAACTATTACCTCTTATCTGGAATGAAGGCTT 2038
 DB 483 AGATGAAATGTAAGTGTGGGCAAACTATTACCTCTTATCTGGAATGAAGGCTT 542
 QY 2039 GAATGATGATCTCTTAAGGCTTTTGTCTCTATGAGAGATG 2081
 DB 543 GAATGATGATCTCTTAAGGCTTTTGTCTCTATGAGAGATG 584

RESULT 14
 A0319961/c 560 bp DNA linear GSS 06-MAY-1999
 LOCUS RPCI11-110F20-TV RPCI-11 Homo sapiens genomic clone RPCI-11-110F20,
 DEFINITION genomic survey sequence.
 ACCESSION A0319961
 VERSION A0319961.1 GI:4052772
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 560)
 Adams,M.D., Rounsfeld,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
 Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
 Use of human BAC End Sequences for Sequence-Ready Map Building
 Unpublished (1998)
 Other_GSSes: RPCI11-110F20-TV
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeec@igrr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong

(pieter@dejong.med.bufile.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.bufile.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.igrr.org/cdb/hungen/bac_end_search/bac_end_search.html
 Seq primer: 586
 Class: BAC ends.

FEATURES

source location/Qualifiers
 1..560
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
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 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"

ORIGIN

Query Match 20.4%; Score 554.8; DB 8; Length 560;
 Best Local Similarity 99.3%; Pred. No. 2.3e-118;
 Matches 556; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 517 TCTTATTAATCTGACTGAAACCTTTTAAAGATATCTGTGTAATTTCCAGTTCTATACGT 576
 DB 560 TCTTATTAATCTGACTGAAACCTTTTAAAGATATCTGTGTAATTTCCAGTTCTATACGT 501
 QY 577 CCTTATGATCTCCGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 636
 DB 500 CCTTATGATCTCCGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
 QY 637 TGAACATCCCTTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 696
 DB 440 TGAACATCCCTTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 381
 QY 697 AGAAGAAAGTGTGATTTCTTACCAAGATGAAAGAAATTTTTCAGAGTGTGTATAT 756
 DB 380 AGAAGAAAGTGTGATTTCTTACCAAGATGAAAGAAATTTTTCAGAGTGTGTATAT 321
 QY 757 AGACACAAACCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 816
 DB 320 AGACACAAACCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261
 QY 817 GAGATGAAACATATTAAGTGTGGCTGCTCTTGTGTTTGAACCAATGATTAATCTTCA 876
 DB 260 GAGATGAAACATATTAAGTGTGGCTGCTCTTGTGTTTGAACCAATGATTAATCTTCA 201
 QY 877 CTGAGAAAGAGAGTTCTTGAAGAAATGTTTAAATTAAGAGAGAGAGAGAGAGAG 936
 DB 200 CTGAGAAAGAGAGTTCTTGAAGAAATGTTTAAATTAAGAGAGAGAGAGAGAGAG 141
 QY 937 CTATGAGACACAAAGAAATTAATTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 996
 DB 140 CTATGAGACACAAAGAAATTAATTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 81
 QY 997 GATGTTTCAATTAATCTTGAACATTTGTCAGAGTTTCAAGAGCTTTCTTTCACAAATTTTCT 1056
 DB 80 GATGTTTCAATTAATCTTGAACATTTGTCAGAGTTTCAAGAGCTTTCTTTCACAAATTTTCT 21
 QY 1057 AGTTGATGATATGAAAAAG 1076
 DB 20 AGTTGATGATATGAAAAAG 1

RESULT 15

BE502913/c 533 bp mRNA linear EST 04-AUG-2000
 LOCUS h281b01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214345 3',
 DEFINITION mRNA sequence.
 ACCESSION BE502913
 VERSION BE502913.1 GI:9705321
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 533)
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncigap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LUM, send email to: info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 487.
 Location/Qualifiers
 1..533
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3214345"
 /issue_type="carcinoid"
 /lab_host="DH10B"
 /clone_lib="NCI-CCGAP Lu24"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CCGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 19.6%; Score 533; DB 2; Length 533;
 Best Local Similarity 100.0%; Pred. No. 2.8e-113;
 Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2184 ATATTTTGTATATGACAGATAATTTTATCTGTCATTACCTTAAAGTCA 2243
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 DB 533 ATATTTTGTATATGACAGATAATTTTATCTGTCATTACCTTAAAGTCA 474

QY 2244 CAGAAAAAATATACATCTTACTCAGGCTTTCTTAAAAATTAATTTTATAGAGATCC 2303
 |||||
 DB 473 CAGAAAAAATATACATCTTACTCAGGCTTTCTTAAAAATTAATTTTATAGAGATCC 414

QY 2304 TTGAGTAAAGACATTTGCTTAATTTCTTTTCTTATCCGACCTGTATATCCCTAC 2363
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 DB 413 TTGAGTAAAGACATTTGCTTAATTTCTTTTCTTATCCGACCTGTATATCCCTAC 354

QY 2364 CAGTACCGGGATCTGCACATCTTTTGAGTTACCTCTTCATAGCAGAAAC 2423
 |||||
 DB 353 CAGTACCGGGATCTGCACATCTTTTGAGTTACCTCTTCATAGCAGAAAC 294

QY 2424 GTTCTATGAGAGACATGCAAGTCAAGCCTCTATTCTGTTAGTACTTATAGAGA 2483
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 DB 293 GTTCTATGAGAGACATGCAAGTCAAGCCTCTATTCTGTTAGTACTTATAGAGA 234

QY 2484 GGAAGATGTTTCATTCATAGAGATTTTCTTACCTTAAGCTTCATAGTACTTA 2543
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 DB 233 GGAAGATGTTTCATTCATAGAGATTTTCTTACCTTAAGCTTCATAGTACTTA 174

QY 2544 CTACTCACTTCCTTTTTCAGTTTTCATATAGTATTCATTTTGGCATATGCTTC 2603
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 DB 173 CTACTCACTTCCTTTTTCAGTTTTCATATAGTATTCATTTTGGCATATGCTTC 114

QY 2604 CTGTAAAGCCAAATTTTATATCTAATTAACATGAACTGCCACTTTCATGCTGCCAA 2663
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 DB 113 CTGTAAAGCCAAATTTTATATCTAATTAACATGAACTGCCACTTTCATGCTGCCAA 54

QY 2664 ACTTGGGGCAATTGATGCTTAAATGCTATTTTAAATATATGTTTTTATCTT 2716
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 DB 53 ACTTGGGGCAATTGATGCTTAAATGCTATTTTAAATATATGTTTTTATCTT 1

Search completed: September 23, 2005, 08:29:10
 Job time : 8591 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using ew model

Run on: September 22, 2005, 23:40:50; Search time 1408 Seconds

(without alignments)
11423.251 Million cell updates/sec

Title: US-10-617-217a-88

Perfect score: 2717
Sequence: 1 aaaaagaacagacagaaagcc.....aataaagcttctattcttc 2717

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_16Dec04:*

1: geneeqn19808:*\n2: geneeqn19908:*\n3: geneeqn20005:*\n4: geneeqn2001as:*\n5: geneeqn2001bs:*\n6: geneeqn2002as:*\n7: geneeqn2002bs:*\n8: geneeqn2003as:*\n9: geneeqn2003bs:*\n10: geneeqn2003cs:*\n11: geneeqn2003ds:*\n12: geneeqn2004as:*\n13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2717	100.0	2717	6	ABQ91955 Human NF- AaT76847 Human sec
2	1835.8	67.6	1860	4	ABQ91955 Human NF- AaT76847 Human sec
3	1337.4	49.2	2171	10	AD030553 Human nov AaK94557 Human ful
4	880.6	32.4	1687	4	AD030553 Human nov AaK94557 Human ful
5	880.6	32.4	1687	12	AD030553 Human nov AaK94557 Human ful
6	476.2	17.5	533	12	AD030553 Human nov AaK94557 Human ful
7	476.2	17.5	533	12	AD030553 Human nov AaK94557 Human ful
8	469.4	17.3	522	10	AD030553 Human nov AaK94557 Human ful
9	243	8.9	253	6	ABN96310 Human nov AaK94557 Human ful
10	156.4	5.8	660	10	AD030553 Human nov AaK94557 Human ful
11	103.6	3.8	104	2	AAK10464 Human col AaK94557 Human ful
12	58.4	2.1	8995	6	ABN46564 Human bpl AaK94557 Human ful
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14	50.8	1.9	5378	6	ABK33879 Human imm AaK94557 Human ful
15	50.8	1.9	10543	6	ABK31249 Human imm AaK94557 Human ful
16	50.8	1.9	10543	6	ABK31249 Human imm AaK94557 Human ful
17	50.8	1.9	10543	6	ABK31249 Human imm AaK94557 Human ful
18	50	1.8	2000	8	ADA71938 Human gen AaK94557 Human ful
19	50	1.8	5586	6	ABK40003 Human che AaK94557 Human ful
20	50	1.8	50000	6	ABK56202 Human che AaK94557 Human ful

ALIGNMENTS

21	49.8	1.8	6876	6	ABK32981 Human imm
22	49.8	1.8	17131	6	ABK33053 Human imm
23	49.4	1.8	11422	6	ABK39937 Human che
24	49.4	1.8	11422	6	ABK32219 Human imm
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26	49.4	1.8	6127	6	ABK34448 Human met
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29	48.4	1.8	2000	8	ADA71938 Human gen
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33	47.4	1.7	34548	6	ABK31432 Human gen
34	47.4	1.7	34548	6	ABK31432 Human gen
35	47.4	1.7	18154	6	ABK44797 Human bpl
36	47.4	1.7	120670	12	AD059167 Human imm
37	46.8	1.7	5418	6	ABK33454 Human imm
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44	46	1.7	415	8	ABK39419 Bovine BS
45	46	1.7	473	10	ABK22180 Breast ca

RESULT 1	ABQ91955	standard; cDNA; 2717 BP.
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AC	30-SEP-2002	(first entry)
DT	Human NF-kB activating gene SEQ ID NO 88.	
DE	Human NF-kB activating gene SEQ ID NO 88.	
XX	Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;	
KW	immunomodulator; cytosolic; antiinfective; osteopathic; nocitropic;	
KW	neuroprotective; anti-HIV; autoimmune disease; cancer; infection;	
KW	bone disease; AIDS; neurodegenerative disease; ischaemic disorder; gene;	
OS	ss.	
XX	Homo sapiens.	
FN	WO200253737-A1.	
XX	11-JUL-2002.	
PD	25-DEC-2001; 2001WO-JP011389.	
PF	28-DEC-2000; 2000JP-00402288.	
PR	26-MAR-2001; 2001JP-00089912.	
PR	24-AUG-2001; 2001JP-00254018.	
XX	(ASAH) ASAH KASEI KOGYO KK.	
PA	Mateuda A, Honda G, Muramatsu S, Nagano Y;	
PI	WPI, 2002-583617/62.	
DR	F-PSDB; ABP61467.	
XX	NF-approximately KB activating gene and expressed protein, applicable in	
PT	diagnosis and screening inhibitors or promoters to control excessive	
PT	activation or inhibition for treating e.g. inflammations, autoimmune	
XX	diseases and cancer.	
PS	Claim 4; Page 403-407; 841pp; Japanese.	
XX	The invention relates to a purified protein (I), comprising one of 90	
CC		

CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF- κ B (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (AB091912-AB092001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and
 CC for treating e.g. inflammations, autoimmune diseases, cancers,
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
 CC disorders
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Sequence 2717 BP; 840 A; 504 C; 541 G; 832 T; 0 U; 0 Other;

Query Match 100.0%; Score 2717; DB 6; Length 2717;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AAATGCTGAGAAATACATAAGTTTCTCTTCTGCTGATATTATTAATGAGTATG 120
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DB 121 GGAAGTCTAAATTAATTCCTGCTCTTCTCTCTTGTGGGTAAAGGACAGATGTG 180
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 DB 2641 TGCCCACTTGTATGATGATCTTACTACTCTCTTTTCAAGTTTCAATATAGTAT 2700
 QY 2701 AAATGTTTTTATTTCTTT 2717
 DB 2701 AAATGTTTTTATTTCTTT 2717

RESULT 2
 ID AAF76847
 AAF76847 standard; cDNA; 1860 BP.

AAAF76847;

14-MAY-2001 (first entry)

Human secreted protein cDNA #5.

Human; secreted protein; immunomodulatory; antileukemic; dermatological;

immunomodulatory; anti-infective; anti-HIV; immunostimulant;

cytotoxic; cardiant; vascular; anti-angiogenic; ophthalmological;

neuroprotective; neurotrophic; anticonvulsant; vaccine; antileishmaniasis;

antiparkinsonian; antimicrobial; vulnary; gene therapy;

immune disorder; hyperproliferative; cardiovascular; angiogenic;

neurological; infection; ss.

XX PN WO200112776-A2.
 XX PD 22-FEB-2001.
 XX PF 15-AUG-2000; 2000WO-US022350.
 XX PR 16-AUG-1999; 99US-0148759P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Shi Y, Young PE, Ebner R, Soppet DR, Ruben SM;
 XX DR WPI; 2001-244245/25.
 XX DR P-PSDB; AAB70066.
 PT Nucleic acids encoding 18 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
 PT and diabetic retinopathy.
 PS Claim 1; Page 350-351; 380pp; English.
 CC The present sequence is one of 18 nucleic acid molecules encoding novel
 CC human secreted proteins. The nucleic acids and proteins may be used in
 CC the prevention, diagnosis and treatment of diseases including immune
 CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and
 CC human immunodeficiency virus (HIV) infections), hyperproliferative
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases
 CC (e.g. Schmitz syndrome, Chaga's cardiomyopathy and coronary
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft
 CC neovascularisation and diabetic retinopathy), neurological disorders
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),
 CC infectious diseases and/or for promoting wound healing, regeneration
 CC and/or chemoradiation. The nucleic acid molecules may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples. The polypeptides may also be
 CC used as antigens in the production of antibodies and in assays to
 CC identify modulators of protein expression and activity
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 Query Match 67.6%; Score 1835.8; DB 4; Length 1860;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1837; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 345 CTCAAATTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 404
 DB 22 CTCAAATTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 81
 QY 405 CTGCTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 464
 DB 82 CTGCTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
 QY 465 AGACAGCATTTTACAGAAATTTAGATGATGATGATGATGATGATGATGATGATGAT 524
 DB 142 AGACAGCATTTTACAGAAATTTAGATGATGATGATGATGATGATGATGATGATGAT 201
 QY 525 CTGACTGAAAACCTTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 584
 DB 202 CTGACTGAAAACCTTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 261
 QY 585 AACTCCGTTTAAAGGAGCATTAATTAACAATCTGTATTAACCATGCGGCGCTGAACAT 644
 DB 262 AACTCCGTTTAAAGGAGCATTAATTAACAATCTGTATTAACCATGCGGCGCTGAACAT 321
 QY 645 CCCCTTCCCGAAGAAAGATCTCCCTTCCCGAAGAAAGATCTCCCTTCCCGAAGAAAGAT 704
 DB 322 CCCCTTCCCGAAGAAAGATCTCCCTTCCCGAAGAAAGATCTCCCTTCCCGAAGAAAGAT 381
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 DB 382 AGTGTGATTTCTTACACAGTAAAGAAATTTTTCAGAGTCTGTATTAAGACACA 441

OY	765	CAAACTAATATGGAAGAGACAAAGAAATATGTAACAAAGACATTTATTTGCTGAGATGAA	824
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OY	825	ACATTAACATATGTGCTGGCTCTTGTATTTGTAAACCAATGATTAATCTTCACTTGAGAA	884
Db	502	ACATTAACATATGTGCTGGCTCTTGTATTTGTAAACCAATGATTAATCTTCACTTGAGAA	561
OY	885	AGCAGTTTCTAGGAAATGTTTAATTAAGAAGAGTCTTCACTTAAGAAACTATGAG	944
Db	562	AGCAGTTTCTAGGAAATGTTTAATTAAGAAGAGTCTTCACTTAAGAAACTATGAG	621
OY	945	CACAGGAAGAAATAATTTCTGAGAGACAGCCATATAAATTTGGTGTACTTTTGAAGTTTC	1008
Db	622	CACAGGAAGAAATAATTTCTGAGAGACAGCTATATAAATTTGGTGTACTTTTGAAGTTTC	681
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OY	1065	GATATGAAGAAAGAAATTTCTCAATCCATATTCCTTTGATTAAGACCTTGAACAAAACTTGT	1122
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OY	1185	ACACAGAAAAAAATATGCCCCCAGAGATCTGATCAACTTCTCTGAGGACCTCTCAT	1244
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Db	1042	TTTTTAAAGAAACCCAGTCAATATGATTTTCGCTGAATTCGCAATTTTGGAGCATTT	1101
OY	1425	CCCAACCAACGATTCACAGCCCATTTGATAGTGTGATGTAGGAGCTTCGTGAGTGTG	1488
Db	1102	CCCAACCAACGATTCACAGCCCATTTGATAGTGTGATGTAGGAGCTTCGTGAGTGTG	1161
OY	1485	TTTCAAGCTCCCCCTGGGGCTTAATCTCTTCATATTAATCATATTTGTAATATAGCTTT	1544
Db	1162	TTTCAAGCTCCCCCTGGGGCTTAATCTCTTCATATTAATCATATTTGTAATATAGCTTT	1221
OY	1545	TATTTGACAGACTTTAAAGGCGTATTAACGTGTGAGTGGCGCATATTCACATTTTAG	1604
Db	1222	TATTTGACAGACTTTAAAGGCGTATTAACGTGTGAGTGGCGCATATTCACATTTTAG	1281
OY	1605	ATCAAAAACTCTCTTATAGAAAGCTTTAAAGTTTCCGTCAACAACAATTCCTCTTCA	1664
Db	1282	ATCAAAAACTCTCTTATAGAAAGCTTTAAAGTTTCCGTCAACAACAATTCCTCTTCA	1341
OY	1665	GAAAGTATTTCAATTAAGTCTTCAAAGTAAGCTGATGTGTGACATGTGTGTGTATTA	1722
Db	1342	GAAAGTATTTCAATTAAGTCTTCAAAGTAAGCTGATGTGTGACATGTGTGTGTATTA	1401
OY	1725	GGTATATTTATTAAGACTTTTGATAGAGAGATGATTTATTAATCTCTATTTCAAGC	1784
Db	1402	GGTATATTTATTAAGACTTTTGATAGAGAGATGATTTATTAATCTCTATTTCAAGC	1461
OY	1785	CCCATGCTCTTCAACAGCCAGAGAGGCCCAACAGATTTGTTTCTTCCCTCCACAGCC	1844
Db	1462	CCCATGCTCTTCAACAGCCAGAGAGGCCCAACAGATTTGTTTCTTCCCTCCACAGCC	1521
OY	1845	TTCTGCCCATTGAGATTTGAGGAGCATCTGTCATTTAGATCAAGGATGGGGTGGAGAA	1904

[illegible]

CC full length human cDNA clone of the invention.

XX Sequence 1687 BP; 458 A; 394 C; 401 G; 434 T; 0 U; 0 Other;

Query Match 32.4%; Score 880.6; DB 12; Length 1687;

Best Local Similarity 99.5%; Pred. No. 76-207; Mismatches 4; Indels 0; Gaps 0;

Matches 883; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

42 TCGCCTGAGATTGAAAGAAATGCTGAGAAATACATAAAGTTTCTCTGCTTGG 101
 801 TGGCCTATTGATGAAAGAAATGCTGAGAAATACATAAAGTTTCTCTGCTTGG 860
 102 ATATTATATATGGGTATCGGAAAGTCTAAATTAATTCCTGCTTCTCTCTGG 161
 861 ATATTATATATGGGTATCGGAAAGTCTAAATTAATTCCTGCTTCTCTCTGG 920
 162 GGTAAAGGACAGATGATGATCAAGTCCAGGATATCAGATGACATTCAGAAAGTCT 221
 921 GGTAAAGGACAGATGATGATCAAGTCCAGGATATCAGATGACATTCAGAAAGTCT 980
 222 GAAGATCTATCTCTGTATATGTTGCTGAGCAAGCAATACACAGAGGGCCACAGCA 281
 981 GAAGATCTATCTCTGTATATGTTGCTGAGCAAGCAATACACAGAGGGCCACAGCA 1040
 282 AAGCAGAGGAGAGCTCAGAGCGTGAAGAGATGTTTGAAGAAAGCTGAAGAGAGTG 341
 1041 AAGCAGAGGAGAGCTCAGAGCGTGAAGAGATGTTTGAAGAAAGCTGAAGAGAGTG 1100
 342 TTCCCTCAATTTGTGATATTCATGAGAAATGACACAGATGAAAGCTCCAGATCCAG 401
 1101 TTCCCTCAATTTGTGATATTCATGAGAAATGACACAGATGAAAGCTCCAGATCCAG 1160
 402 AATCTGCTACAGATGATGATGATCAACCCGGAATATCTTGGCTGAGATGCCATGT 461
 1161 AATCTGCTACAGATGATGATGATCAACCCGGAATATCTTGGCTGAGATGCCATGT 1220
 462 GGCAGACAGCATTTACAGATTTAGATGCTGTAATGGTCTGATGACATCTTA 521
 1221 GGCAGACAGCATTTACAGATTTAGATGCTGTAATGGTCTGATGACATCTTA 1280
 522 TTACTGACTGAAATCTTTTAAAGATCTTGTGTAATTCAGTTCATATCGTCCCTA 581
 1281 TTACTGACTGAAATCTTTTAAAGATCTTGTGTAATTCAGTTCATATCGTCCCTA 1340
 582 ATGAATCTCGTTAAGAGGACGATTAATCAACTCTGTATACCATGCGGCCCTGAAC 641
 1341 ATGAATCTCGTTAAGAGGACGATTAATCAACTCTGTATACCATGCGGCCCTGAAC 1400
 642 AATCCCTTCCCGGAGAAAGACTCCCTTGGCTCCCAACATCATGCTTTAGAGAA 701
 1401 AATCCCTTCCCGGAGAAAGACTCCCTTGGCTCCCAACATCATGCTTTAGAGAA 1460
 702 GAAATCTGAGATTTCTTACAGATGAGAAAGATTTTTCAGAGTCTGTATTAAGACA 761
 1461 GAAATCTGAGATTTCTTACAGATGAGAAAGATTTTTCAGAGTCTGTATTAAGACA 1520
 762 CAACAACATATATGAGAAAGACAAGAAATATGTATCAAGACAAATTTATGCTGAGAT 821
 1521 CAACAACATATATGAGAAAGACAAGAAATATGTATCAAGACAAATTTATGCTGAGAT 1580
 822 GAAACATATATATGAGAAAGACAAGAAATATGTATCAAGACAAATTTATGCTGAGAT 881
 1581 GAAACATATATATGAGAAAGACAAGAAATATGTATCAAGACAAATTTATGCTGAGAT 1640
 882 GAAACATATATGAGAAAGACAAGAAATATGTATCAAGACAAATTTATGCTGAGAT 928
 1641 GAAACATATATGAGAAAGACAAGAAATATGTATCAAGACAAATTTATGCTGAGAT 1687

RESULT 6
 ID AAK93015/C
 AAK93015 standard; cDNA; 533 BP.

AAK93015;
 06-NOV-2001 (first entry)
 Human cDNA 3'-end sequence, SEQ ID NO: 1475.
 Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
 Homo sapiens.
 EP1330094-A2.
 05-SEP-2001.
 07-JUL-2000; 2000BP-00114089.
 08-JUL-1999; 99JP-00194486.
 11-JAN-2000; 2000JP-0018774.
 02-MAY-2000; 2000JP-00183765.
 (HELI-) HELIX RES INST.
 Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 WPI, 2001-52425/58.
 830 Primers useful for synthesizing full length cDNA clones and their use
 in genetic manipulation.
 Claim 3; SEQ ID NO 1475; 1380bp + Sequence Listing; English.
 The invention relates to primers for synthesizing full length cDNA
 clones. 830 cDNA molecules encoding a human protein have been isolated
 and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 been determined. Primers for synthesizing the full length cDNA are useful
 for clarifying the function of the protein encoded by the cDNA. The full
 length clones were obtained by construction of full length enriched cDNA
 libraries that were synthesized by the oligo-capping method. The primers
 enable the production of the full length cDNA easily without any special
 methods. The present sequence is the nucleotide sequence of the 3'-end of
 a cDNA provided in the invention. Note: The sequence data for this patent
 did not form part of the printed specification, but was obtained in CD-
 ROM format directly from EPO

Sequence 533 BP; 150 A; 103 C; 89 G; 175 T; 0 U; 16 Other;

Query Match 17.5%; Score 476.2; DB 4; Length 533;
 Best Local Similarity 93.4%; Pred. No. 3-4e-107;
 Matches 498; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

396 GTCCAGATCTGCTCAAGATGATGATGATCAACCCGGAATATCTTCTGAGATG 455
 532 GTCCAGATCTGCTCAAGATGATGATGATCAACCCGGAATATCTTCTGAGATG 473
 456 CCATGTGACAGACAGCATTTACAGAAATTAAGATGCTGTAATGGTCTGATGAGACA 515
 472 CCATGTGACAGACAGCATTTACAGAAATTAAGATGCTGTAATGGTCTGATGAGACA 414
 516 ATCTTATATCTGATGAGAAATCTTTTAAAGATCTTGTGTAATTTCCAGTTCATATAG 575
 413 ATCTTATATCTGATGAGAAATCTTTTAAAGATCTTGTGTAATTTCCAGTTCATATAG 354
 576 TCCCTAATGAATCTCGTTAAGAGGACGATTAATCAACTCTGTATACCATGCGGCC 635
 353 TCCCTAATGAATCTCGTTAAGAGGACGATTAATCAACTCTGTATACCATGCGGCC 294
 636 CTGAACATATCTTCCCGGAGAAAGACTCCCTTGGCTCCCAACATCATGCTTTA 695
 293 ATGAACATATCTTCCCGGAGAAAGACTCCCTTGGCTCCCAACATCATGCTTTA 234
 696 GAGGAAGAAATGCTGATTTCTTACACAGTATGAGAAAGATTTTTCAGAGTCTGTAT 755

```

Db      233 GAGGAGAAAGTGTGATTTCTTACACAGTAGAAGAAATTTTCAGAGTCTGTGNAT 174
QY      756 AAGACACAACTATCTATGGAAGAGAGAAATATGTTACAAAGCAATTTATGGC 815
Db      173 AAGACACAACTATCTATGGAAGAGAGAAATATGTTACAAAGCAATTTATGGC 114
QY      816 TGAGATGAAACATATACATGTGGCTGGCTGTGTTTGTAAACCAATGATTAATCTTC 875
Db      113 TGAGATGAAACATATACATGTGGCTGGCTGTGTTTGTAAACCAATGATTAATNTTC 54
QY      876 ACTTGAGAAAGCACTTTCTAGGAATGTTTAAATAAAGAGTCTTCACCTT 928
Db      53 ACTTGAGAAAGCACTTTTGAAGAAATGTTTAAATAAAGAGTTCACCTT 1

RESULT 7
ADL29442/c
ID      ADL29442 standard; cDNA, 533 BP.
XX
AC      ADL29442;
XX
DT      20-MAY-2004 (first entry)
XX
DE      3' end of a human cDNA molecule SegID 1475.
XX
KW      human; medicine; signal transduction; glycoprotein; transcription;
KM      oligo-capping method; ss.
XX
OS      Homo sapiens.
XX
PN      EP1396543-A2.
XX
PD      10-MAR-2004.
XX
PF      07-JUL-2000; 2003EP-00025638.
XX
PR      08-JUL-1999; 99JP-00194486.
PR      11-JAN-2000; 2000JP-00118774.
PR      02-MAY-2000; 2000JP-00183865.
PR      07-JUL-2000; 2000EP-00114089.
XX
PA      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI      Ota T, Nishikawa T, Isogai T, Hayashi S, Iehi S, Kawai Y,
PI      Makematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR      WPI; 2004-204755/20.
XX
PT      New oligonucleotide primers (830 CDNAe) useful for synthesizing full
XX      length human CDNAe.
XX
PS      Disclosure; SEQ ID NO 1475; 1340bp; English.
XX
CC      This invention relates to a novel primers useful for synthesizing full
CC      length cDNA molecules that encode human proteins. Specifically, it refers
CC      to secretory or membrane proteins that are potential therapeutic agents/
CC      target molecules in the field of medicine, and in particular genes
CC      encoding proteins that are associated with signal transduction,
CC      glycoproteins and transcription. The present invention describes a method
CC      for efficiently cloning a full length human cDNA from both the 5' and 3'
CC      ends using the oligo-capping method. This polynucleotide sequence is the
CC      3' end of a full length human cDNA sequence of the invention.
XX
SQ      Sequence 533 BP; 150 A; 103 C; 89 G; 175 T; 0 U; 16 Other;
Query Match 17.5%; Score 476.2; DB 12; Length 533;
Beet Local Similarity 93.4%; Pred.No.3.4e-107;
Matches 498; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
QY      396 GTCCAGAACTCTCTACAGATGACTTGGTATCAAAACCGGAAATATCTTCTGAGATG 455
Db      532 GTTCAGATTTGMAAAGGAGAAATGTGATATCAACCCGGATTAATTTTGTGATGATG 473

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QY      456 CCATGTGGCAGACAGCATTTTACAGAAATTTAGATGATGCTGTAATGGTCTGCAATGACA 515
Db      472 CCATGTGGCAGACAGCATTTTACAGAAATTTAGATGATGCTGTAAT-GGTCTGCAATGACA 414
QY      516 ATCTTATTAATGACTGAAACCTTTTAAAGATACCTTGTTGTTTCCAGTTCTATACG 575
Db      413 ATTTTATTAATGACTGAAACCTTTTAAAGAAATCTGTTGTTTCAAGTTTNNATACG 354
QY      576 TCCCTTAATGAATCCCGTTTAAAGGAGATTAATTAACAATCTGTTATACCATGGGGCC 635
Db      353 TCCCTTAATGAATCCCGTTTAAAGGAGATTAATTAACAATCTGTTATACCATGGGGCC 294
QY      636 CTGAACAAATCCCGTTTCCCGGAGAAAGACTCCCTTTGGCCCTCAAAACCATGAATGCCCTTA 695
Db      293 ATGAACAAATCCCGTTTCCCGGAGAAAGACTCCCTTTGGCCCTCAAAACCATGAATGCCCTTA 234
QY      696 GAGGAGAAAGTCTGTGATTTCTTACACAGTAGAAGAAATTTTTCAGAGTCTGTGNAT 755
Db      233 GAGGAGAAAGTGTGATTTCTTACACAGTAGAAGAAATTTTTCAGAGTCTGTGNAT 174
QY      756 AAGACACAACTATCTATGGAAGAGAGAAATATGTTACAAAGCAATTTATGGC 815
Db      173 AAGACACAACTATCTATGGAAGAGAGAAATATGTTACAAAGCAATTTATGGC 114
QY      816 TGAGATGAAACATATACATGTGGCTGGCTGTGTTTGTAAACCAATGATTAATCTTC 875
Db      113 TGAGATGAAACATATACATGTGGCTGGCTGTGTTTGTAAACCAATGATTAATNTTC 54
QY      876 ACTTGAGAAAGCACTTTCTAGGAATGTTTAAATAAAGAGTCTTCACCTT 928
Db      53 ACTTGAGAAAGCACTTTTGAAGAAATGTTTAAATAAAGAGTTCACCTT 1

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RESULT 8
ADC32380
ID      ADC32380 standard; cDNA, 522 BP.
XX
AC      ADC32380;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Human novel cDNA contig sequence, SEQ ID NO:2462.
XX
KW      Human; diagnostic; drug screening; forensics; gene mapping;
KW      biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW      neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW      ulcers; osteoporosis; autoimmune disease; cancer;
KW      molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW      neuroprotective; anti-inflammatory; anticoagulant; thrombolytic; vulnary;
KW      antitumor; osteopathic; immunosuppressive; antiinflammatory; cyostatic;
KW      gene therapy; chromosome 5; ss.
XX
OS      Homo sapiens.
XX
PN      WO2003029271-A2.
XX
PD      10-APR-2003.
XX
PF      24-SEP-2002; 2002WO-US030474.
PR      24-SEP-2001; 2001US-0324631P.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Tang TY, Zhang J, Ren F, Xue AJ, Zhao QX, Wang J, Wehrman T;
PI      Zhou P, Ghoosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI      Haley-Vicente D, Dimaucac RT;
XX
DR      WPI; 2003-371981/35.
DR      P-PsDB; ADC33147.
XX
PT      New polynucleotide and polypeptide useful for diagnosing, preventing or
XX      treating conditions such as neurodegenerative diseases, anemia, platelet

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OY      2652 CATGCTGCGCAAACTGGGCAATTGATGTAATGTTTAAATAAATGTTTAA 2711
DB      66 CATGCTGCGCAAACTGGGCAATTGATGTAATGTTTAAATAAATGTTTAA 7
OY      2712 TTCTTT 2717
DB      6 TTCTTT 1

RESULT 10
ACD94489/C
ID      ACD94489 standard; cDNA; 660 BP.
AC      ACD94489;
XX
XX
DT      23-SEP-2003 (first entry)
DE      Human colon cancer cell expressed cDNA #2901.
KW      Open reading frame detection; genome sequencing; colon cancer;
KW      breast cancer; population genome analysis; genetic shift; cancer;
KW      antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW      agriculture; food crop genome; resistance gene; retrovirus;
KW      influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW      gene; ss.
XX
XX      Homo sapiens.
XX
XX      US2002155438-A1.
XX
XX      24-OCT-2002.
XX
XX      27-SEP-1999; 99US-00406117.
XX
XX      20-NOV-1998; 98US-00196716.
XX
XX      (SIMP/) SIMPSON A J G.
XX      (NETO/) NETO E D.
XX      (BREN/) BRENTANI R R.
XX
XX      Simpson AJG, Neto ED, Brentani RR;
XX
XX      WPI; 2003-182626/18.
XX
XX      Determining open reading frames of genome of an organism e.g. a human
XX      suffering from cancer involves use of single oligonucleotide primer at
XX      low stringency for preparing single-stranded cDNA from mRNA of
XX      individual.
XX
XX      Example 9; Page 430; 959pp; English.
XX
XX      The invention describes a method of determining open reading frames in
XX      the genome of organism, comprising contacting mRNA from cell of organism
XX      with a single oligonucleotide primer (I) at low stringency, preparing
XX      single-stranded cDNA by reverse transcribing mRNA with (II), amplifying
XX      cDNA, sequencing the product, and repeating the contacting, preparing
XX      and amplifying steps with different primers and sequencing resulting
XX      nucleic acids. The method is useful for: determining that a known
XX      nucleotide sequence from a genome of an organism corresponds to a
XX      nucleotide sequence of an open reading frame; for preparing a contig,
XX      nucleic acid molecule from a genome of an organism; and for sequencing
XX      all or part of a genome of an organism. mRNA is obtained from mammalian
XX      or human cell which is associated with a pathological condition e.g. a
XX      colon cancer or breast cancer cell. The method is useful for analyses of
XX      populations of subjects and can be used to carry out genetic analyses of
XX      large or small populations. further, it can be used to study living
XX      systems to determine if, e.g. there have been genetic shifts which render
XX      an individual or population more or less likely to be afflicted with
XX      diseases such as cancer, to determine antibiotic resistance or non-
XX      tolerance, and so forth. The method can also be used in the study of
XX      congenital diseases, and the risk of affliction to a fetus, as well as
XX      the study of whether the conditions are likely to be passed to offspring

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CC      through ova or sperm. The analyses for pathological conditions can be
CC      carried out in all animals, plants, birds, fish, etc. Using this method,
CC      in the area of agriculture, for example the genomes of food crops can be
CC      studied to determine if resistance genes are present, defects in plant
CC      genomes can also be studied in this way. Similarly, the method permits
CC      determination of the pathogens which integrate into the genome, such as
CC      retroviruses and other integrating viruses such as influenza virus, have
CC      undergone shifts or mutations, which may require different approaches to
CC      therapy. This method is also applied to eukaryotic pathogens, such as
CC      trypanosomes, different types of Plasmodium, etc. The method essentially
CC      eliminates sequencing of non-coding portions. This sequence represents a
CC      polynucleotide isolated from human colon cancer cell cDNA library
XX
XX      SQ
XX      Sequence 660 BP; 180 A; 139 C; 156 G; 180 T; 0 U; 5 Other;
XX
XX      Query Match      5 8%; Score 156.4; DB 10; Length 660;
XX      Best Local Similarity 73.6%; Pred. No. 3.7e-28;
XX      Matches 270; Conservative 0; Mismatches 82; Indels 15; Gaps 5;
XX
OY      2309 TAAAGACATTTTGGCTTAATTTCTTTTCTTAATTCCTCCACTGTATATCCCTACAGTA 2368
DB      538 TAAAGTCTGAGAGCATTTGCTATTTCTTTTCTATCCCACTGTATATCCCTCAGT- 480
OY      2369 CCGGATCTGACACATCTTTTGGAGTTTACCTTTCATAGCCATGAACCAAAAGCTTT 2428
DB      479 -CGGATCTGACACATCTTT---GCAGTACCTCTTATAGCCATG-ACCCAAAGTTC 426
OY      2429 ATGAGGACATGCAAGTATGCAAGCCCTCATTCGTATGACTTATTAAGAGAGAGA 2488
DB      425 AT-AGGACATGCAAGTATGCAAGCCCTCATTCGTATGACTTATGACTTGA------GAGA 374
OY      2489 TGGTTTCATTGCAATGATGACATTTTCTTAGCCTTAACGTTCTGATAGTACTACT 2548
DB      373 TGGTTTCATTGCAATGATGACATTTTCTTAGCCTTAACGTTCTGATAGTACTACT 314
OY      2549 CACTTCTCTTTTTCAGTTTTCATATATAGTATTCATTTTGGCATATAGTCTCTGTA 2608
DB      313 CACTTCTCTTTTTCAGTTTTCATATATAGTATTCATTTTGGCATATAGTCTCTGTA 254
OY      2609 AAGCCATTTTATATCTATATAAACATGAACGACCTCTTCATGCTGCGCAACTTG 2668
DB      253 AAGCCATGATCTCTGCGACCGGACGACCATTTGGACCGAATTCACCTTAAACAAG 194
OY      2669 GGGCAAT 2675
DB      193 CCGCAAT 187

RESULT 11
AAAX10464/C
ID      AAAX10464 standard; DNA; 104 BP.
XX
XX      AAAX10464;
XX
XX      30-MAR-1999 (first entry)
XX
XX      Human biallelic polymorphic DNA fragment WI-11806.
XX
XX      Polymorphism; biallelic; human; forensic; paternity testing; disease;
XX      detection; phenotypic typing; characteristic; infection; hereditary;
XX      autoimmune disease; cancer; inflammation; drug; therapy; medicament;
XX      treatment; marker; ss.
XX
XX      Homo sapiens.
XX
XX      WO9820165-A2.
XX
XX      14-MAY-1998.
XX
XX      05-NOV-1997; 97WO-US020313.
XX
XX      06-NOV-1996; 96US-0030455P.
XX

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 02:09:46 ; Search time 445 Seconds
(without alignments)
9990.481 Million cell updates/sec

Title: US-10-617-217A-88

Perfect score: 2717
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50.8	1.9	1141	US-09-806-708B-22	Sequence 22, Appl
2	50.6	1.9	1141	US-09-806-708B-22	Sequence 22, Appl
3	49.8	1.8	7218	US-08-232-463-14	Sequence 14, Appl
4	48.6	1.8	7218	US-08-232-463-14	Sequence 14, Appl
5	47.8	1.8	55195	US-09-949-016-15854	Sequence 15854, A
6	47.8	1.7	601	US-09-949-016-54021	Sequence 54021, A
7	47.7	1.7	601	US-09-949-016-54022	Sequence 54022, A
8	47.7	1.7	601	US-09-949-016-54022	Sequence 54022, A
9	47.7	1.7	601	US-09-949-016-54022	Sequence 54022, A
10	47.7	1.7	601	US-09-949-016-108655	Sequence 108655, A
11	47.7	1.7	601	US-09-949-016-108656	Sequence 108656, A
12	47.7	1.7	104520	US-09-949-016-108658	Sequence 108658, A
13	47.7	1.7	126029	US-09-949-016-14731	Sequence 14731, A
14	46.6	1.7	601	US-09-949-016-54023	Sequence 54023, A
15	46.6	1.7	601	US-09-949-016-108657	Sequence 108657, A
16	45.4	1.7	601	US-09-949-016-54020	Sequence 54020, A
17	45.4	1.7	601	US-09-949-016-108654	Sequence 108654, A
18	45.2	1.7	19438	US-09-949-016-12699	Sequence 12699, A
19	45.2	1.7	103988	US-09-949-016-12513	Sequence 12513, A
20	45.2	1.7	103988	US-09-949-016-17050	Sequence 17050, A
21	44.8	1.6	45587	US-09-949-016-15836	Sequence 15836, A
22	44.6	1.6	146401	US-09-949-016-16151	Sequence 16151, A
23	44.6	1.6	15236	US-09-949-016-17517	Sequence 17517, A
24	43.6	1.6	44353	US-09-949-016-15302	Sequence 15302, A
25	43.6	1.6	50381	US-09-949-016-17122	Sequence 17122, A
26	43.6	1.6	58597	US-09-949-016-13598	Sequence 13598, A
27	43.6	1.6	58597	US-09-949-016-13598	Sequence 13598, A

C	28	43	1.6	832	4	US-09-621-976-2813	Sequence 2813, Ap
C	29	43	1.6	317366	4	US-09-949-016-16001	Sequence 16001, A
C	30	42.8	1.6	1055	4	US-09-806-708B-23	Sequence 23, Appl
C	31	42.8	1.6	331814	4	US-09-949-016-12008	Sequence 12008, A
C	32	42.8	1.6	331814	4	US-09-949-016-17056	Sequence 17056, A
C	33	42.6	1.6	601	4	US-09-949-016-151811	Sequence 151811, A
C	34	42.6	1.6	1939	1	US-07-715-751B-2	Sequence 2, Appl1
C	35	42.4	1.6	55264	4	US-09-949-016-15014	Sequence 15014, A
C	36	42.4	1.6	94755	4	US-09-949-016-11839	Sequence 11839, A
C	37	42.4	1.6	119153	4	US-09-949-016-12378	Sequence 12378, A
C	38	42.2	1.6	1455	4	US-09-917-265A-104	Sequence 104, App
C	39	42.2	1.6	1455	4	US-09-917-265A-106	Sequence 106, App
C	40	42.2	1.6	250715	4	US-09-949-016-13294	Sequence 13294, A
C	41	42	1.5	152132	4	US-09-949-016-13845	Sequence 13845, A
C	42	42	1.5	152145	4	US-09-949-016-12371	Sequence 12371, A
C	43	41.8	1.5	1055	4	US-09-806-708B-23	Sequence 23, Appl
C	44	41.8	1.5	64081	4	US-09-790-988-1	Sequence 1, Appl1
C	45	41.6	1.5	6265	3	US-09-129-112-3	Sequence 3, Appl1

ALIGNMENTS

```
RESULT 1
US-09-806-708B-22/c
/ Sequence 22, Application US/09806708B
/ Patent No. 6784342
/ GENBANK INFORMATION:
/ APPLICANT: The University of British Columbia
/ TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
/ FILE REFERENCE: 4810-58741
/ CURRENT APPLICATION NUMBER: US/09/806,708B
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: US 60/147,133
/ PRIORITY FILING DATE: 1999-08-04
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 22
/ LENGTH: 1141
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (1)..(1141)
/ OTHER INFORMATION: consensus sequence of A.C., L.a., and B.N. FAEI promoters
US-09-806-708B-22

Query Match      1.9%; Score 50.8; DB 4; Length 1141;
Best Local Similarity 10.8%; Pred. No. 0.0012;
Matches 81; Conservative 279; Mismatches 390; Indels 3; Gaps 1;

QY 945 CACAGAGAAAGTAATTTCTGACGAGACCTATAAAATGTGACTTTTGAATGCTTC 1004
   ::::::::::::::::::::: : :::::::::::::::::::::
DB 860 YHHAAKRWKMMWRTITNNNNNNNNNNACRNTTWWABKSHWCNNNNNNNNNNNTWC 801
   ::::::::::::::::::::: : :::::::::::::::::::::
QY 1005 AGTAACTGACATGTCAGAGTTCAGAGACTTTTCTTCAATTTCTAGTTCATG 1064
   ::::::::::::::::::::: : :::::::::::::::::::::
DB 800 HTTANABBCVRANNNNAABMATTCNNWAAATTTHTDCCYKRWMTTWDMWTMBT 741
   ::::::::::::::::::::: : :::::::::::::::::::::
QY 1065 GATATGAAAAAGAAATTCATTCATTCATTCCTGTTATTTGAACCTTGACAAAACTGT 1124
   ::::::::::::::::::::: : :::::::::::::::::::::
DB 740 TTTATGTTTSTMTNNNNNNNNNNWACNNNNNNNNNNKAYAHATNNMGCWMNTTARFRNTTV 681
   ::::::::::::::::::::: : :::::::::::::::::::::
QY 1125 ATGACAGACATTTTAAATATGACCAACCTTTATTTCTGTAATTTTGAATTCGAAG 1184
   ::::::::::::::::::::: : :::::::::::::::::::::
DB 680 WRRKMTNTYKTRWSTTRRHHTYATNNNNNNNNNNNNNNNNNSCTCTRWMTTMTMGD 621
   ::::::::::::::::::::: : :::::::::::::::::::::
QY 1185 ACACAGAAAAAATGAGCCAGAGATGATGATCACTTCCTGAGGACCTCTCAT 1244
   ::::::::::::::::::::: : :::::::::::::::::::::
DB 620 GMTATRKVKRRDITCTYVDWADSWVMWYANWMBGRVITRRNTYCKSYAHSYWYNN 561
   ::::::::::::::::::::: : :::::::::::::::::::::
QY 1245 GGATGTTGCAATTAAGCACTTGCGGTACTATCAACCAAGAAATATGATTTCCAGAAATAGAAC 1304
   ::::::::::::::::::::: : :::::::::::::::::::::
```

Db 560 AMWYRYSARWSSWABWTRNNMWSGBVWRWAGTMMWRHNNNTDTRYMMWKMA 501
 Oy 1305 ATTTGACATGTTAAGCGTTGATGATATATAATCGAATAGATGGAATGSGAAC 1364
 Db 500 RBTITVYSMCNAKSMRGNMRAKMMWAAANDADHDHMYMNNNTMMWRBAMKMN 441
 Oy 1365 TTTTAAAGAACCAGTCAAAATGATTTTGTGGAATCGCATATTTGAGGACATTT 1424
 Db 440 MAMCRALCCNNNNRACVNHGKMRRTKMKAKACNNNBKAMTRVAMMTSRDT 381
 Oy 1425 CCCACACGATTCAG---CCCATTTGATAGTGTGATAGGACGTTGSGAGTG 1481
 Db 380 NTDMMWTSDBMHMYTVDYTWBRAMNNNNNNNNNNBCKTSMWMMMDHNTCTGNWTM 321
 Oy 1482 GTGTTCAAGCGTCCCGGGGCTTAAATCTCTTCAATATGATGATCTTGAATAGG 1541
 Db 320 GSAYBMAAMSMWAGASNBVTYNNWCMRTYMGKTNNNNNNKAYYRTKTVAMCNRYY 261
 Oy 1542 CTTTATTTGACAGGCTTCAAAAGCGTATACTGTGAGTGGCCAGATATTCATTTT 1601
 Db 260 YDTAVMTKRYKTYATVBYWYBMGKHMBWRABHRSNNMMWVCRAKMYMSWTH 201
 Oy 1602 TAGATCAAAAACCTCTTATAGAGCTTTAAAGTTCCGACACACAATCTCTCT 1661
 Db 200 AMRYBKABAVGCNNNMKDRMAHHMWCATNNNNMMWYAYMHHMKKGAATNNKTABR 141
 Oy 1662 CAGAGATATTTCTCATTTAGTCTTCAAGTA 1694
 Db 140 DDBAHVKTYYWRYDWCAMCMWNAKAKVRTA 108

RESULT 2

; Sequence 22, Application US/098067088
 ; Patent No. 6784342
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of British Columbia
 ; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
 ; FILE REFERENCE: 4810-58741
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/147,133
 ; PRIOR FILING DATE: 1999-08-04
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 1141
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; NAME/KEY: Promoter
 ; LOCATION: (1)..(1141)
 ; OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. FAE1 promoters
 US-09-806-7088-22

Query Match 1.9%; Score 50.6; DB 4; Length 1141;

Best Local Similarity 9.9%; Pred. No. 0.0014; Mismatches 412; Indels 5; Gaps 1;

Oy 1840 AGCCCTTGTCCCATCTGAGATGAGGAGCATGCTTCACTTGAGATGAGGATGGGCTG 1899
 Db 62 ARMYCKRYRWYNNKSRMKWYKKMYCBANNTSRYABRABKDKMTYABMTMKMGKT 121
 Oy 1900 GAGATGGGTATGATGATGATGAGAAAAGCCCTTCCGGATCATGAGATTTGTTCT 1959
 Db 122 GWRHRYWYMRABDVTVDHYYVAMNNAMTTTMCMDKDRRTFWWKKNNATGMDDTKY 181
 Oy 1960 AGTCAATTTCTGCACATGAGATGAATGATGATGAGGCAACATATTTACCTCTCTTA 2019
 Db 182 HMMNNNGBYTWMYRYKTRDRMSKRNMYGBMMKMSYDVTYYMMWMDCKRKYRW 241
 Oy 2020 TCTGTGAATGAAGGGTGAATGATGATCTTAAAGGCTTTTGTCTCTATGAGAT 2079

Db 242 VRTGBRYWVAMBTAHRRRYNNGWTBAMAYRRRTMNNNNNNNAKAMCKRKYMGMBAB 301
 Oy 2080 GTGAAAA-----CTAGGACCAACAAAAGGAACAAGAAAAAGTTTGATTCATATAA 2134
 Db 302 VNSCTTWSKXTTYKRSVCMANNCRADANDHMKWKSAAAGYNNNNNNNTYTKAR 361
 Oy 2135 GTGATATGTAATAGTGCAGAGGCTTATATATATGCTTATATGATAAAGATATTTTTGT 2194
 Db 362 HBAAWDMVMBAMKMAAAAHYRKQWBYRKRTYNNNNNTTMMKSMVAYMGMDMW 421
 Oy 2195 ATATGACAGATATATTTATTTTAAATGCTGTGATTAACATTAAGATCAAGAAAAAA 2254
 Db 422 BGYNNNNNGRTYTGWTKNNKQWMTYYKMKANNCKMBMDHKTCTHNTTMMKTYWNN 481
 Oy 2255 TATACATGCTTACGACGCTTCTTAAAAAATAATTTTATAGAGATCTTGATTAAGA 2314
 Db 482 CYWKSMTNGSHRBAALVYTWMMWRYYAANNNDYMKACTWYKYBVCISKWNYYA 541
 Oy 2315 CATTTGCTTATATTTCTTTTCTTATTCCTTATTCCTTATTCCTTACAGTACCGGA 2374
 Db 542 AMYTKSMNTSRYYRMTKNNNSMRSDTSMGBANNYABABHYGKMTTMBWBSHTMB 601
 Oy 2375 TCTGCACATCTTTTGGAGTACCTCTTCATAGCCATGAACAAAAGTTTATGAGG 2434
 Db 602 HBRAGAHYWMBWYBAKCHCMKAMYAKKYAGAGSGSNNNNNNNNNNNNNNATCARD 661
 Oy 2435 AGCATGCAAGTAATCAAGCTCTTATCTGTAATTAAGAGAGAGATGTTT 2494
 Db 662 YYASRYAMANAAYYKYBAANNAVYTHANNMGCMMNATDTRTKNNNNNNNAGTWK 721
 Oy 2495 TCATGATAGTGCATTTCTTGTAGCTTACGTTGATAGTACTTACTTCACTTC 2554
 Db 722 NNNNNNAKMSAAKGYAAAYAKAKGMRMANKMAAGMHDAABTTDKNNNGAYTKYT 781
 Oy 2555 TCTTTTCACTTTCATATATAGATTCATTTTGGCATTAAGCTTCCGTGAAGCA 2614
 Db 782 TTNNNNTYRGVYTTAARDGANNNNNNNNNNNNNNNGSDMWYTWAAVAGTNNNNNN 841
 Oy 2615 ATTTATATCTAATAAACAAT 2636
 Db 842 NNAAYAMTKMYTTTDDRMB 863

RESULT 3

; US-08-232-463-14
 ; Sequence 14, Application US/08232463
 ; Patent No. 3670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,463
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935,313
 ; FILING DATE:
 ; APPLICATION NUMBER: EP 91 114 300.6

```

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZpc-F18
US-08-232-463-14

Query Match          1.8%, Score 48.6; DB 1; Length 7218;
Best Local Similarity 0.8%; Pred. No. 0.015;
Matches    3; Conservative 216; Mismatches 140; Indels   0; Gaps   0;

QY      160 GGGGTAAAGCAGCATGCTGATCAACGTCAGATATCATGATTCAGATTCCAGAAGT 219
        ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1422 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1363

QY      220 CTGAAGATCTACTCTTGTAATGTGCTGAGCAGACGAATCAACAGAGGGGCCAACG 279
        ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1362 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1303

QY      280 GAAGCGAGGAGGAGCTCAGCGCTGCAAGAGATGTTGAAGAAAGCTGAAGAGAG 339
        ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1302 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1243

QY      340 GTTCTCAATTTGTGATTTGATGATGCAGAAATGACACAGATGAAGCCCTCAGATCC 399
        ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1242 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1183

QY      400 AGAATCTGCTACAAGATGACTTTGGTATCAACC CGAATAATCTTTGCTGAGATGCCAT 459
        ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1182 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1123

QY      460 GTGCGACACAGCATTTACGAATTTAGATGATGCTGTAATGGCTGATGATGACATC 518
        ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1122 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1064

RESULT 5
US-09-949-016-15854/C
Sequence 15854, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH TYPE II DIABETES WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
```

```

: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 15854
: LENGTH: 55195
: TYPE: DNA
: ORGANISM: Human
: OS-09-949-016-15854

```

Query Match	1.8%;	Score 47.8;	DB 4;	Length 55195;
Best Local Similarity	53.5%;	Pred. No. 0.085;		
Matches 100;	Conservative 0;	Mismatches 87;	Indels 0;	Gaps 0;

Accession	Sequence	Position
Oy	2084 AAAAATCTGGGGCCCAAAAGGAAACAAGCAAAAAAGTTTGATTCGATTAAGGATATCT	2143
Db	19373 AAAATGAGGCGCAAAAAGATGAAAAAAGAAACAAGTTTAAATGGGCAAAAGAAATTA	19314
Oy	2144 AATAGTTGCAGAGGCTTTATATATGCTTAAATGAAAGATTTTTTGTATATTGACA	2203
Db	19313 CTAACTTGATGTGATGATGAATTCACCTCTATTAAACAATTCGATGAATGCAATGGTTT	19254

QY 2209 GCCTAATTATTTTAACTGTCATACACTAAAGTCACAGGAAAAATATCATGC 2265
Db 1253 GAACATCTCAATTTAAAAGCTCAGATAAATTTAAAGATATATCATCAAAATTTAAAGA 13194

Qy	2265	TTACTCA	2270
Db	19193	TATATCA	19187

```

RESULT 6
US-09-949-016-54021
; Sequence 54021, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 54021
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-54021

```

Query Match	1.7%	Score 47;	DB 4;	Length 601;
Best Local Similarity	51.7%	Pred. No. 0.0095;		
Matches 107; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

[illegible]

QY	2250	AAAAATATACATGCTTACTACAGCCTTCTTAAAAATAAATTTTATAGAGATCCTTGAGT	23050
Db	285	TATATAATATATATATAATATAATATAATATAATATAATATAATATAATATAAT	344

QY 2310 AAAGACATTTTGCTTAATTTCTTTT 2336
||| | ||| | ||| |||||

Db 345 AAATATATATATAATTTTTTTTT 371

RESULT 7
US-09-949-016-54022

```

: Patent No.6812339
:
: GENERAL INFORMATION:
:
: APPLICANT: VENTER, J. Craig et al.
:
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
:
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
:
: FILE REFERENCE: CLO001307

```

1 CURRENT APPLICATION NUMBER: US/09/949,016
 2
 3 CURRENT FILING DATE: 2000-04-14
 4
 5 PRIOR APPLICATION NUMBER: 60/241,755
 6
 7 PRIOR FILING DATE: 2000-10-20
 8
 9 PRIOR APPLICATION NUMBER: 60/237,768
 10
 11 PRIOR FILING DATE: 2000-10-03
 12
 13 PRIOR APPLICATION NUMBER: 60/231,498

```

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54022

```

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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-54022

```

Query Match	1.7%	Score 47;	DB 4;	Length 601;
Best Local Similarity	51.7%	Pred. No. 0.0095;		
Matches 107; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0

OY	2130	ATAAAGGATATGTAAATAGTCGGAAAAGCCTTATATATGCTTTTAAAGAAAAGTATT	2188
D6	160	ATAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	219
OY	2190	TTTGATATTTGACAGCAATTAATTTTTTAAATGCTGCATTACACTTAAAGTCACAGAA	2245
D6	220	TACTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	279
OY	2250	AAAAATATACATGCTTACTCAGGCTTTCTTAAAAATAAATTTTATAGAGATCCTTGAGT	2305
D6	280	TATATAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	339
OY	2310	AAAGACATTTGCTTAATTTCTTTTT	2336
D6	340	AAATATATATTAATTAATTTTTTTTTT	366

```

RESULT 8
US-09-949-016-54024
; Sequence 54024, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54024
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-54024

```

```
Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 2130 ATAAAGTATGTATAGTTCGAGAGGCTTTATATAGCTTATATGAAAAGATATT 2189
Db 95 ATATATATAATATATATATATATATATATATATATATATATATATATATATAT 154
Qy 2190 TTGTATATGACAGCATATTTTATTTTAACTGCTTCACTTAAGTCACAGAA 2249
Db 155 TACATATATATATATATATATATATATATATATATATATATATATATATAT 214
Qy 2250 AAAAATATATCATGCTTACTCAGGCTTTCTTAAAAATATTTTATAGAGATCCTTGACT 2309
Db 215 TATATAATATATATATATATATATATATATATATATATATATATATATAT 274
Qy 2310 AAAGCATTTTGCTTAATTTCTTTT 2336
Db 275 AAATATATATATATATATATTTT 301

RESULT 9
US-09-949-016-108655
; Sequence 108655, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108655
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108655

Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 2130 ATAAAGTATGTATAGTTCGAGAGGCTTTATATAGCTTATATGAAAAGATATT 2189
Db 165 ATATATATAATATATATATATATATATATATATATATATATATATATATAT 224
Qy 2190 TTGTATATGACAGCATATTTTATTTTAACTGCTTCACTTAAGTCACAGAA 2249
Db 225 TACATATATATATATATATATATATATATATATATATATATATATATATAT 284
Qy 2250 AAAAATATATCATGCTTACTCAGGCTTTCTTAAAAATATTTTATAGAGATCCTTGACT 2309
Db 285 TATATAATATATATATATATATATATATATATATATATATATATATATAT 344
Qy 2310 AAAGCATTTTGCTTAATTTCTTTT 2336
Db 345 AAATATATATATATATATTTT 371

RESULT 10
US-09-949-016-108656
; Sequence 108656, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
```

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108656
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108656

Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 2130 ATAAAGTATGTATAGTTCGAGAGGCTTTATATAGCTTATATGAAAAGATATT 2189
Db 160 ATATATATAATATATATATATATATATATATATATATATATATATATATAT 219
Qy 2190 TTGTATATGACAGCATATTTTATTTTAACTGCTTCACTTAAGTCACAGAA 2249
Db 220 TACATATATATATATATATATATATATATATATATATATATATATATATAT 279
Qy 2250 AAAAATATATCATGCTTACTCAGGCTTTCTTAAAAATATTTTATAGAGATCCTTGACT 2309
Db 280 TATATAATATATATATATATATATATATATATATATATATATATATATATAT 339
Qy 2310 AAAGCATTTTGCTTAATTTCTTTT 2336
Db 340 AAATATATATATATATATTTT 366

RESULT 11
US-09-949-016-108658
; Sequence 108658, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108658
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108658

Query Match 1.7%; Score 47; DB 4; Length 601;
Best Local Similarity 51.7%; Pred. No. 0.0095;
Matches 107; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 2130 ATAAAGTATGTATAGTTCGAGAGGCTTTATATAGCTTATATGAAAAGATATT 2189
Db 95 ATATATATAATATATATATATATATATATATATATATATATATATATATAT 154
```


[illegible]

```

RESULT 12
US-09-949-016-13303
/ Sequence 13303, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CLO001307
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13303
/ LENGTH: 104520
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(104520)
/ OTHER INFORMATION: n = A,T,C or G
/ US-09-949-016-13303

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[illegible]

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14731
LENGTH: 126029
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(126029)
OTHER INFORMATION: n = A,T,C OR G
US-09-949-016-14731

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[illegible]

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1         RESULT 14
2         US-09-949-016-54023
3         Sequence 54023, Application US/09949016
4         Patent No. 681239
5         GENERAL INFORMATION:
6         APPLICANT: VENTER, J. Craig et al.
7         TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
8         TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
9         FILE REFERENCE: C0001307
1        CURRENT APPLICATION NUMBER: US/09/949,016
12       CURRENT FILING DATE: 2000-04-14
13       PRIOR APPLICATION NUMBER: 60/241,755
14       PRIOR FILING DATE: 2000-10-20
15       PRIOR APPLICATION NUMBER: 60/237,768
16       PRIOR FILING DATE: 2000-10-03
17       PRIOR APPLICATION NUMBER: 60/231,498
18       PRIOR FILING DATE: 2000-09-08
19       NUMBER OF SEQ ID NOS: 207012
20       SOFTWARE: FastSeq for Windows Version 4.0
21       SEQ ID NO 54023
22       LENGTH: 601
23       TYPE: DNA
24       ORGANISM: Human
25       US-09-949-016-54023

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	Query Match	Similarity	Score	DB #	Length	Gaps
Best Local Similarity	51.2%	Pred.	No. 0.012;			
Matches	106;	Conservative	1;	Mismatches	100;	Incls 0
Qy	2130 ATAAAGTATGTGTAATGGTTGCAGAACGCTTTATTATTCCTTATATATGAAGAAGATATTT					2188
bD	156 AATAAATATTAATATATTAATAAAAATAATATATATATTAATAATATATATTAATAAAAAA					215

